GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
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Listing first 45 summaries
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## ALIGNMENTS

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A;Gene: SGD:SUP35; SUF12; GST1; SUP2; MIPS:YDR172w A;Gross-references; SGD:S0002579; MIPS:YDR172w A;Map position: 4R C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology C;Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; F;1-123/Domain: A CDM1> F;42-119/Region: 10-residue repeats F;124-253/Domain: charged <dom2> F;124-253/Domain: charged <dom2> F;124-253/Domain: dutamic acid/lysine-rich F;254-685/Domain: C CDM4&gt; F;261-409/Domain: translation elongation factor Tu homology <etu> F;367-274/Region: nucleotide-binding motif A (P-loop) F;406-409/Region: GTP-binding NKXD motif</etu></dom2></dom2>	A; Molecule type: DNA A; Residues: 1-685 < MUR> A; Cross-references: EMBL: 246727; NID:g1289283; PIDN:CAA86677.1; PID:g128A; Cross-references: EMBL: 246727; NID:g1289283; PIDN:CAA68760.1; PIDN:CAA68760.1; PIDN:CAA68760.1; C:Genetics: DNA A; Residues: 1-52, 'C', 54-685 < KIK> A; Cross-references: GB:Y00829; EMBL:Y00859; NID:g3711; PIDN:CAA68760.1; C:Genetics:	EMBL:X07163; NID:94581; PIDN:CAA30155.1; P: BEND:X07163; NID:94581; PIDN:CAA30155.1; P: BEND:X0800000000000000000000000000000000000	
Tu homology hosphoprotein; tan	PID:g1289287; GSPDB:G es a protein containin 68760.1; PID:g3712	(D:94582 SV, A.P.; Smirnov, V.N. comyces cerevisiae. PID:9172791	rotein YDR172w Jan-2001 

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RESULT
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A;Title: The complete sequence of a 11,953
A;Reference number: S17471; MUID:91377317
A;Actession: S17471
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hypothetical protein YCL028w - yeast (Saccharomyces cerevisiae)
hypothetical protein YCL181

%; Alternate names: hypothetical protein YCL181
C; Species: Saccharomyces cerevisiae
C; Pate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 29-Oct-1999
C; Accession: S19355; S17471; C27061
R; Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, K.; Ramezani Rad, M.; Xu, submitted to the Protein Sequence Database, March 1992
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A; Residues: 1-180, 'T', 182-322, 'VHSQLWLPWQVPTWAITPIQIRVMGASNRLMSMVDRN', 'RMVNSNPMSTEDRNTAI
A; Cross-references: EMBL:M16717; NID:g171534; PIDN:AAA34615.1; PID:g171536
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A:Tille: Two genes required for cell fusion during A:Reference number: A93093; MUID:87286864
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A; Residues: 1-186 <RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S19350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: S58084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
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                                                                                                                                                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                        2 SDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSG------
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                                                    SFSALASMASSYLGNNSNSNSSYGGQQQANEYG-RPQHNG
                                                                                                                                             ----YQQGGYQQYNPDAGYQQQYNPQG---GYQQYNPQG-----GYQQQFNPQG---
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Pred. No. 1.
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Pred.
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1. No. 4.2e-54;
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                                                                                                                                                                                                                                                     DB 2;
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S71954
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                                                                                                                                                                                                                                                                                                   Genetics
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Best Local
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                      56
                                                                                                                               Local
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                                                    _
                                                                                                                                             Match
                                                                                                                                                                                                                                                                                     taf68
                    QQ----
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A;Description: required for activated transcription; binds RNA and single c;Superfamily: RNA-binding protein EWS; ribonucleoprotein repeat homology C;Keywords: RNA binding C;Keywords: RNA binding F;232-307/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology C;Keywords: GTP binding; nucleotide binding; P-loop; phosphoprotein F;319-467/Domain: translation elongation factor Tu homology <ETU> F;325-332/Region: nucleotide-binding motif A (P-loop) F;464-467/Region: GTP-binding NKXD motif F;331/Binding site: GTP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kushnirov, V.V.; Ter-Avanesyan, M.D.; Didichenko, S.A.; Smirnov, V.N.; Chernoff, Yeast 6, 461-472, 1990
Yeast 6, Vergence and conservation of SUP2(SUP35) gene of yeasts Pichia pinus and A;Title: Divergence and conservation of SUP2(SUP35) gene of yeasts Pichia pinus and A;Reference number: S12921; MUID:91181341
A;Accession: S12921
                                                                                                                                                                                                                                                                                                                                                                                                                              C; Complex: up to 13 TATA-binding protein-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:x56910; NID:g3235; PIDN:CAA40231.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-589 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: hTAFII68, a novel RNA/ssDNA-binding protein with homology A;Reference number: S71954; MUID:97045110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S71954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA/ssDNA-binding protein TAFII68 - human
N;Alternate names: TATA-binding protein-associated factor TAFII68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-741 < KUS>
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N; Alternate names: SUP2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X98893; NID:g1628402;
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;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 02-Feb-2001
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                                                                                                      1 MSDS----NQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPA-GGYYQNYQGYSGY 55
                                                    MSDSGSYGQSGGEQQSYSTYGNPGSQGYG----QASQSYSGYGQTTDSSYGQNYSGYSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQEQQFGQYGQQQQNYNQ-GGYNNYNNR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i, A.; Lutz, Y.;
5022-5031, 1996
                                                                                                                                                                                      Similarity
                                                                                                                                                             Conservative
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-GGY--
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Pred. No. 2.9e-07;
7; Mismatches 36
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                                                                                                                                                             Pred. No. 3.8e-07
3; Mismatches 4
                                                                                                                                                                                                                 Score 163.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.J.; Chambon,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA67398.1;
                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                 factors (TAFIIs) form together
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                                                                                                                                                                                                                    589;
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DAG protein homolog Fibra.iv Characters: Arabidopsis thallana (mouse-ear cress) C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04886 C;Accession: T04886
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                                                                                                                                                                                                                                                                   A; Dicture type: DNA A; Molecule type: DNA A; Residues: 1-409 <WIL>
A; Residues: 1-409 <WIL>
A; Cross-references: EMBL: Z69383; PIDN: CAA93412.1; GSPDB: GN00022; CESP: F13E9.4
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A; Residues: 1-419 <BEV>
A; Cross references: EMBL: AL021637
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R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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A; Introns: 32/1; 275/3; 337/3
                                                                                                                                                                                                                                                                                                                                                                                                            R:MCMurray, A. submitted to the EMBL Data Library, February 1996 A;Reference number: Z19332 A;Accession: T20847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F13E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T20847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 123/2;
A; Note: F18F4.120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z15388
A; Accession: T04886
                                                                                                                                                                                                                                                             A; Gene: CESP:F13E9.4
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                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 - AGYNQGQGSPVPPYQAGYNQVQGSPVPPYQGTQSSYG-QGGSGNYSQGPQGGYNQGGPR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 QNFQRNTQYGQQPPMQGGGGSYGPQQGYATPGQGQGTQAPPPFQGGYNQGPRSPPPPYQ- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 QFNPQGGRGNYKNFNYNNNL------QGYQAGFQPQSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 YSGYQQG-----GYQQYN-----PDAGYQQQYNPQGGYQQYN--PQGGYQQ---- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 QNYQQYSQNGNQ---QQGNNRY---QGY----QAYNAQAQP--AGGYYQN-----YQG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                           Local Similarity es 48; Conserv
                                                              4 SNOGNNOONYOO-YSONGNOOOGNNRYOGYOAYNAOAOPAGGYYON-----YOGYSGYO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGYDQH--QGSYDEQSN-----YDQQHDSYSQNQQSYHS 148
                      TGQGLLESSYQQGYGQNQGSMQGYSQ----QGYGGNSQQDYGYSQSQGSGMGVQGYGGSS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQSYSQSYGGYENQKQSSYSQQPYNNQGQQQNMESSGSQGGRAPSYDQPDYGQQDSYDQQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156/1; 178/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cultivar Columbia; BAC
                                                                                                                             21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.1%;
                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 148; DB 2;
Pred. No. 6.1e-06;
9; Mismatches 42
                                                                                                         Score 147.5; DB 2
Pred. No. 6.6e-06;
5; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone F18F4
                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                           Indels
                                                                                                                                                   Length 409;
                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-Oct-1999
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                         8
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円
                                                                                                                                                                                                                                                                          N; Alternate names: synexin
N; Contains: annexin VII, short form
C; Specites: Dictyostelium discoideum
C; Date: 30-Sep-1992 #sequence_revision 30-Sep-C; Accession: S14723; S22756; A40977; A38670
R; Greenwood, M; Tsang, A.
Biochim. Biophys. Acta 1088, 429-432, 1991
A; Title: Sequence and expression of annexin VI
A; Reference number: S14723; MUID: 91198150
A; Accession: S14723
               A:Molecule type: mRNA
A:Residues: 17-462 <GRE2>
A:Cross-references: EMBL:X60270; NID:g7209; PI
A:Cross-references: EMBL:X60270; Noegel, A.A.
J. Biol. Chem. 266, 17509-17515, 1991
A:Title: Dictyostelium annexin VII (synexin).
A:Reference number: A40977; MUID:91373375
A:Accession: A40977
                                                                                                                                                                                            A;Cross-references: EMBL:X60269
A;Accession: S22756
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-339 < GRE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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A; Introns: 15/3; 53/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z69791; PIDN:CAA93660.1; A;Experimental source: clone F39D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-945 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A; Reference number: 219499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Ainscough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F39D8.1a - Caenorhabditis elegans
C;Species: Caenorhabditis, elegans
C;Date: 15-Oct-1999  #sequence_revision 15-Oct-1999  #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annexin VII - slime mold (Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F39D8.la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T21998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 NAGGYYDQNQFQGQDQNINAGGYYGNQNQNPGQFQDQNQNNYQGQYQGSTLAPSAGEVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 OSYGOO----AFAQQQRPQQGFQSNGFSGQQASGSMNSFGGQGGYGQNQNGFGGQSGFS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNA-QAQ---PAGGYYQNY-QGYSGY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-----NFNYNNNLQGY--QAGFQPQSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOSGWGSNSLSSANSNGNNN-QGSSSGYQ-NNQG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQGGYQQYNPDAGYQQQYNPQG--GYQQYNP-----QGGYQQQFN-----PQGGRGNY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGDQNQNQFQDPNQGQYQNQNQNINTGGYIGDQSQNQNQGQYPDPNQGQYQNQNQNQNI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPETPSGNTDYNNNAQGFDQQQGQQGQYQ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGGYQQYNPDAGYQQQYNPQGGYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T21998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89/1; 109/3; 363/1; 741/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NENYNNNLOGYQAGFQPQSQG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 147.5; DB 2
Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      on 30-sep-1992
A38670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discoideum
                                                                                                                               PIDN:CAA42816.1;
                                                                                                                                                                                                                                                                                                                           VII of
                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OYNPOGGYQQQFNPQGGRGNYK 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881/3;
                                                              sequence
                                                                                                                                                                                                                                                                                                                         Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                          #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               904/1;
                                                                and
                                                                                                                             PID:g671859
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discoideum

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G:Genetics:
A;Gene: DdANN7
C;Superfamily: annexin VII; annexin repeat homology
C;Keywords: alternative splicing; calcium binding; calcium chann
F;1-462/Product: annexin VII *status predicted <MAT1>
F;1-462/Product: annexin VII *status predicted cymatics
F;1-513/Region: 6-residue repeats (Q-Q-G-Y-P-P)
F;164-235/Domain: annexin repeat homology <AXI>
F;175-191/Region: endonexin fold
F;318-391/Domain: annexin repeat homology <AX2>
F;247-863/Region: endonexin fold
F;318-391/Domain: annexin repeat homology <AX3>
F;395-462/Domain: annexin repeat homology <AX4>
F;406-422/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-8,52-46
A; Cross-references: (
R; Gerke, V.
J. Biol. Chem. 266,
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                                                                                                                                                                                                                                      A;cross-reterences: EMBL:Z74032; NID:el061692; PIDN:CAA98466.1; GSPDB:GN00023; CESP:F35FA;Experimental source: clone F35B12 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F35B12.3 - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21735 R;White, S. submitted to the EMBL Data Library, June 1996 A;Reference number: Z19466
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A;Recession: A38670
A;Recession: A38670
A;Molecule type: protein
A;Residues: 143-155;176-185;192,'X',194-197,'X',199;217-222;264-272;302-305;347-360;431
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholi
                                                                                                                                                                               A; Map position:
A; Introns: 129/2
                                                                                                                                                                                                               A; Gene: CESP:F35B12.3
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                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-232 <WIL>
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                            A; Accession: T21735
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Best Local S
Matches 55
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                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
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            GNNQQNYQQYSQ--NGNQQQGNNRYQGYQAYNAQAQPAGGY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGY---QQYNPDAGY--QQQYNPQGGY---QQYNPQGGY--QQQFNPQGGRGNYKNFNYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQGYPPQSNSPQPGQYGAPQQGYPPQQGYPPQQGY----PPQQGYPPQQGYPPQQGYPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOG-NNOQNYQQYSQNGNQQQGNNRYQGY---QAYNAQAQPAGGY--YQNYQGYSGY-QQ
                                                                          50;
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QGYPPQQGYPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                               20.5%;
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                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 147; DB 1;
Pred. No. 8.3e-06;
2; Mismatches 40
                                                                                               Score 144;
Pred. No. 7
                                                                          Mismatches
                                                                                             DB 2;
.5e-06;
                                                                          46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462
                                                                                                                Length
                                 ----YQNYQGYSGYQ-
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
              232;
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                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      duplication;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                          10;
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RESULT
S41022
F;445-516/Domain: annexin F;528-600/Domain: annexin F;604-675/Domain: annexin
                                                           C; Superfamily: annexin repeat homology F; 373-444/Domain: annexin repeat homol
                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-676 <BER>
                                                                                                                                                                                                                 A; Reference number: A; Accession: $41022
                                                                                                                                                                                                                                        submitted to the EMBL Data A; Reference number: S41014
                                                                                                                                                                                                                                                                                             hypothetical protein T07C4.9 - Caenorha C; Species: Caenorhabditis elegans C; Date: 06-Jan-1J95 #sequence_revision C; Accession: S41022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not A;Molecule type: DNA A;Residues: 1-372 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma
A;Reference number: A64200; MUID:96026346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.; Fuhrmann, J.; Nguyen, C.A.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: I6'
R; Fraser, C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bifunctional endo-1,4-beta-xylanase homolog - Mycoplasma genital C;Species: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                  A; Introns: 69/3; 161/1; 208/3;
                                                                                                                     C; Genetics:
                                                                                                                                       A; Cross-references: EMBL: Z29443; NID: g1067051; PID: g443836
                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                               R; Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Genetic code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U39699; GB:L43967; NID:g1045903; PID:g1045904; TIGR:MG217
A;Experimental source: strain G-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: 164223
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 NQQQFNQPSFDLNNQ-QFNQPGFNQSPAFEITPQEQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 QGGRGNYKNENYNNNLQGYQAGEQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 PNQQQFNQPGFDPNQQYYQDPNQQQFN-QAGFDQNQYYQDPNQQQFNQSGFDQNQYYQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 DQNQYYQDPNQQQFNQSGFDPNQQQFNQPGFDPNQQYYQDPNQQQFNQAGFDQNQQYYQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DSNQGNNQQNYQQYSQNG---NQQQGNN----RYQGYQAYNAQAQPAGGYYQNYQGYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQGGQRGYQ---GYQSNQRSQGSYPERYDSSMYSPVMDLTNYYGSQGTPQYYGYPSSASY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNYDQQYSQQSQYYPSSGQQG----YRG--GYQSNPGMQGGYQGNGQDSYQDFQGYQGYQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -OGGYQQYNPDAGYQQQYNPQGGYQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 32.7
51; Conservative
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annexin repeat homology <AX1>
annexin repeat homology <AX6>
annexin repeat homology <AX3>
annexin repeat homology <AX4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GY--QQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQSQG
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D.; Utterback, '
                                                                                                                                                                                                                                                          Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -YQQGGYQQYNPDAGY-QQQYNPQGGYQQYNPQGGYQQQF--NP
                                                                                                227/1; 357/1; 505/3
                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 143; DB 2;
Pred. No. 1.5e-05;
2; Mismatches 55;
                                                                                                                                                                                                                                                                                                                      06-Jan-1995
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T.R.; Saudek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shown;
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                                                                                                                                                                                                                                                                                                                  #text_change 09-Sep-1997
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D.M., Phi
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Phillips,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
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Length 676;

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dsRNA-binding protein 4F.2 - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C:Accession: 11653
R:Bass, B.L.; Hurst, S.R.; Singer, J.D.
Curr. Biol. 4, 301-314, 1994
A:Title: Binding properties of newly identified Xenopus proteins
                                                                                                                                                    RESULT
I51653
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A:Title: Identification of novel genes, SYT and SSX, involved in the t(X:18)
A:Reference number: S46269; MUID:95038836
A:Accession: S46269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision
C;Accession: S46269; S51172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
S46269
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A; Residues: 'M', 15-404 <COO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cooper, C.S.
submitted to the EMBL Data
A;Reference number: S51172
A;Accession: S51172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-404 <CLA>
A;Cross-references: EMBL:X79201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:434322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:SSXT; SYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X79201;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     MGQVNQGNHMMGQRQIPPYRPPQQGPPQQYSGQEDYYGDQYSHGGQGPPEGMNQQYYPDG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQQPSYGGYGQPPQQPGYGNGSYDPYGQPQQQPYPGGGGQPPYPGSNSNQGGGGYPGQGG 289
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                                                                                                                                                                                                                                                                                                                                                                                                       MSDSNQGNNQQNYQQY-----SQNGNQQQ--GNNRYQGYQ-AYNAQAQPAG----GYYQNY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQQYNPDAGYQQ - - QYN - - - -
                                                                                                                                                                                                                        PQG---QGQQYGGYRPTQPG
                                                                                                                                                                                                                                                          NYNNNLOGYQ-AGFQPQSQG 123
                                                                                                                                                                                                                                                                                              NSQYGQQQDAYQGPPPQQGYPPQQQQYPGQQGYP----
                                                                                                                                                                                                                                                                                                                                 QGYSGYQQGGYQQYNPDAGY---QQQYNPQGGYQQYNPQGGYQQQFNP-QGGRG-NYKNF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
properties of newly identified Xenopus
er: IS1652; MUID:95006648
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141; DB 2; Pred. No. 2.4e-05; 9; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 142; DB 2; Pred. No. 3.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 404;
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                   proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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                   containing
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                    dsRNA-bindir
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hypothetical protein At2g25960 (imported) - Arabidopsis thallana K, Alternate names: hypothetical protein T19L18.23 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change C; Accession: T02627; H84654 R; Rounsley, S.D; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L. submitted to the EMBL Data Library, August 1998 A; Description: Arabidopsis thaliana chromosome II BAC T19L18 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T18240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U07156; NID:g463904; PIDN:AAA19961.1; PID:g514260 C;Superfamily: double-stranded RNA-binding repeat homology F;303-371/Domain: double-stranded RNA-binding repeat homology <DSR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-800 <BASS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Note: Ca49C4.01
A;Note: Ca49C4.01
C;Superfamily: WW repeat homology
F;10-48/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDB.
A;Molecule type: DNA
A;Residues: 1-236 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Barrell, B.G.; Rajandream,
submitted to the EMBL Data Li
A:Reference number: Z18831
A:Accession: T18240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical transmembrane protein - yeast (Candida C;Species: Candida albicans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
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A; Status: prelimina
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nes 45; Conserv
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31.9%; Pred. No. 1.56
tive 12; Mismatches
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Pred. No. 4.9e-05;
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A;Gene: T19L18.23; At2g25960
A;Map position: 2
A;Introns: 112/1; 206/3; 240/3; 264/3; 304/3
C;Superfamily: glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: H84654
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-632 <STO>
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A:Experimental source: cultivar Columbia
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
Nature 402, 761-768, 1999
Search completed: February 1, Job time: 217 sec
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A;Accession: T02627
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-632 <ROU>
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                               2002, 15:02:47
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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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                                                                  COUNTRY: USAN
ZIP 80803

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compattible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PALENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,391
FILLNG DATE: 13-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
REGISTRATION NUMBER: 33.878
REFERENCE/DOCKET NUMBER: 93-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEPTA: (303) 499-8080
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-391-2
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US-08-749-391-2
                      Query Match 17.3
Best Local Similarity 35.3
Matches 49; Conservative
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A Xylanase TITLE OF INVENTION: Anaerobic F
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STREET: 53
CITY: Boul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boulder
STATE: Colorado
COUNTRY: USA
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Hu, Youji
Forsberg, Cecil W.
Moloney, Maurice M.
Moloney, A Xylanase
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Liu, Jin-Hao
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US-08-619-554-2
US-08-619-56-9788-61
US-08-793-331-4
US-08-793-331-4
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US-08-793-712-1
US-08-793-712-1
US-08-793-771-1
US-08-733-731-1
US-08-733-731-1
US-08-733-731-1
                    Score 121; DB 2;
Pred. No. 0.00013;
8; Mismatches 55;
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US-09-390-200-2
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                                                                                                                                                                      Query Match
Best Local Similarity
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Patent No. 613703
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hu, Youji
APPLICANT: Forsberg, Cecil W.
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: A Xylanase Obtained From
TITLE OF INVENTION: Anaerobic Fungus
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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         361 QGGSPWGG-NQGGNPWGGNQGGSPWGGNQGGSPWGQGNQGGNPWGGNQGGSPWGGNQGGN 419
                                                                           304 QGNDQQG-QQPPQGQQPPQGNDQQQCQQPPQPQGPQGGNPGGSDFNNWNQG--GSPWGGN 360
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                                          61 QQYNPDAGYQQQYNPQGGYQQYNPQGGYQ------QQFNPQGGR------GNYKNF 104
                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Donna M. Ferber REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                 6 QGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQ----AQPAGGYYQNY-QGYSGYQQGGY 60
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                                                                                                                                                                                                                                                                                               amino acid
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Hu, Youji
                                                                                                                                                       Conservative
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Liu, Jin-Hao
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35.5%;
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                                                                                                                                                    Score 121; DB 4; Length 485;
Pred. No. 0.00013;
8; Mismatches 55; Indels
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US-07-982-112-2

; Sequence 2, Application US/07982112

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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: BODENMULLER, Heinz
APPLICANT: DESSAUER, Andreas
TITLE OF INVENTION: METHOD FOR THE DETECTION OF A SMALL
TITLE OF INVENTION: CELL LUNG CARCINOMA
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO:
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 899301
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NAME: Luther, Barbara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700.
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MEDIUM TYPE: Diskett
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APPLICANT: Stuart, Susan G.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                             274 PQGDYGQQGYGPQGAPTSFSN 294
                                                                                                                                                                                                                                                                 224 EKQPAPG---DAYGDAGYGQGPGGY----
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                                                                                                                                                                                                                             84 PQGGY-QQQFNPQGGRGNYKN 103
                                                                                                                                                                                                                                                                                  NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: 296 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                 Score 111.5; DB 2;
Pred. No. 0.00065;
6; Mismatches 19;
                                                                                                                                                                                                                                                                 -GPQDSYGPQGGYQPDYGQPAGSGGSGYG 273
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                   Length 296;
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CORRESPONDENCE ADDRESS:
Nikaido, Marmelstein, Murray & Oram

655 Fifteenth Street N.W. Suite 330

NUMBER OF SEQUENCES:

CITY: Washington

STREET:

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; MOLECULE TYPE:
US-07-982-112-2
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Approximately 10 5670317
                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5670317
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/617,102
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Chin, Monica F.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 564-1906
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC TITLE OF INVENTION: SMALL ROUND CELL TUMOR
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Landanyi, Marc APPLICANT: Gerald, William
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 EKQPAPG---DAYGDAGYGQGPGGYGPQDSYGPQGGYQPDYGQPASGGGGYGPQGDYGQQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 GYGQQGAPTSFSN 305
                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 QFNPQGGRGNYKN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 QAQPAGGYYQNYQGYSGYQQ--GGY---QQYNPDAGYQQQY-NPQGGYQQYNPQGGY-QQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                          10036
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20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08437027
                                                                                                                                                                                                                     1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                            Cooper & Dunham LLP
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US/08/437,027
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US-08-437-027-20
; Sequence 20, Application US/08437027
; Patent No. 5670317
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; MOLECULE TYPE: US-08-437-027-20
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC toOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: LILL STREET: New York
CITY: New York
TMATE: New York
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REFERENCE/DOCKET NUMBER: 46.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: unl
MOLECULE TYPE:
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGN
TITLE OF INVENTION: SMALL F
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NAME: White, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                              STRANDEDNESS: unkr
TOPOLOGY: unknown
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                                                                                                                                                                                       NAME: White, John P
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 QTTATYGQTAYATSYGQPPTGYTTPTAPQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 QYNPQGGYQQY-----NPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 NYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQ 71
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                 LENGTH:
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10036
                                                                 amino acid
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                                                                                 365 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMALL ROUND CELL TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
                                                                                                                                                                                                                                                                                                US/08/437,027
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                                                                                                                                                                                        46416/JPW/CCA
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Pred. No. 0.0052;
4; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                  Version
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US-08-343-443B-2
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Patent No. 596873
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Best Local Similarity
                                                                                         TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ZUCMAN, JESSICA
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: AEDIT 1.0 DO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                     NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 230 South... CITY: Philadelphia
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/FR93/00494 FILING DATE: 19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 QTTATYGQTAYATSYGQPPTGYTTPTAPQA-----YSQPVQGYGTG 96
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                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19102
                                 amino acid
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230 South Fifteenth Street
                                                     656 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Peter, Martine
Ploougastel, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delattre, Olivier
Desmaze, Chantal
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                                                                                                                                   215-875-8383
                   linear
protein
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                                                                                                                                                                                     19,763
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Pred. No. 0.0052;
""matches 48;
                                                                                                                                                                         989.6121P
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Query Match

14.8%;

Score 103.5;

DB 2;

Length 656;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Sharp, Phil
APPLICANT: Zhou, Qiang
                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08538711A Patent No. 5994062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.8%;
Best Local Similarity 31.8%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09214564A Patent No. 6150515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/214,564A CURRENT FILING DATE: 1999-08-18 PRIOR APPLICATION NUMBER: US 60/021,218 PRIOR FILING DATE: 1996-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional TITLE OF INVENTION: Elongation By HIV-1 TAT FILE REFERENCE: M0656/7042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                APPLICANT: MULSHINE, TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 NYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQ 71
OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                               COUNTRY: U
ZIP: 10154
                                                                                                                                                       CITY: NEW YORK
                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 QYNPQGGYQQY-----NPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAG 116
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                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                 NEW YORK
                                                                                                                                                                         345 PARK AVENUE
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                                                                                                                                                                                                                                , JAMES, L.
AN EPITHELIAL PROTEIN AND
DNA THEREOF FOR USE IN EARLY CANCER DETECTION
23
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                   PC-DOS/MS-DOS
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4; Mismatches
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; TYPE: Amino Acid
; STRANDEDNESS: Unkn
; TOPOLOGY: Linear
; MOLECULE TYPE: pepti
US-08-538-711A-8
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US-08-725-027-8
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REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08725027 Patent No. 6251586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MULSHINE, JAMES, L.
APPLICANT: TOCKNAN, MELVYN, S.
TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
NUMBER OF SEQUENCES: 23
                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                       APPLICATION NUMBER: US08/538,711
FILING DATE: 02-OCT-1995
ATTORNEY_AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 02-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
STATE: NEW YORK
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                                                                            2026-4201US1
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Pred. No. 0.0054;
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US-08-538-711A-7
US-08-538-711A-7
; Sequence 7, Application US/08538711A
; Patent No. 5994062
; Patent No. 5994062
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                                                                                                                                              ; MOLECULE TYPE: peptide US-08-538-711A-7
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Best Local Similarity
                                                        Matches
                                                                                         Query Match
                                                                                                                                                                                                                                                                                TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Unknow
TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MULSHINE, JAMES, L.
TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GGGY-----GGGYDNYGGGNYGSGNYNDFGNYNQQPSNY
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                                              Local Similarity 33.3%;
hes 33; Conservation
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18 QNGNQQQGNNR--YQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNP 75
                                                                                                                                                                                                  TYPE: Amino Acid
STRANDEDNESS: Unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/O
FILING DATE: .02-OCT-1995
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                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                       Linear
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                                                                                                                                                                                                      Unknown
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                                                                          Score 103; DB 2;
Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                            2026-4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103; DB 4;
Pred. No. 0.0054;
                                                        Mismatches
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                                                      44; Indels 16;
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                                                                                       Length 353;
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Matches Query Match

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RESULT 13
US-07-814-964-13
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US-08-725-027-7
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                                                          Sequence 13, Application US/07814964 Patent No. 5359047
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                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/538,711
FILING DATE: 02-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
   APPLICANT:
                  APPLICANT:
                                APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                               228
                                                                                                                                                  280 GGGY-----GGGYDNYGGGNYGSGNYNDFGNYNQQPSNY 313
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                                                                                                                                                                             76 QGGYQQYNPQGGYQQQENPQGGRGNYKNF-NYNNNLQGY 113
                                                                                                                                                                                                                                18 QNGNQQGNNR--YQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNP 75
                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
STRANDEDNESS: Un
TOPOLOGY: Linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Donahue, Brian A.
Toney, Jeffrey H.
Bruhn, Suzanne L.
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TOCKMAN, M
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Pred. No. 0.0056;
6; Mismatches 4
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                                                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                      US-08-258-442-13
                                                                                                                       RESULT 14
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                                                                        Sequence 13, Application US/08258442 Patent No. 5670621
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                            GENERAL INFORMATION:
             APPLICANT:
APPLICANT:
                                           APPLICANT:
   APPLICANT:
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Donahue, Brian /
Toney, Jeffrey !
Bruhn, Suzanne !
Pil, Pieter M.
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TELEPHONE: 617-861-624
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0: FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: 2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA Structure Specific Recognition TITLE OF INVENTION: Protein and Uses Therefor NUMBER OF SEQUENCES: 13
123 SVTGTGASSNNNSNNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                    95 Q-GGRGNYKNFNYNNN 109
                                                                               63 QYANSNSNNNVNVNALPQDFGYMQQTGSGQNYPTINQQQFSEFYNSFLSHLTQKQTNP 122
                                                                                                                  51 GYSGYQQGGYQQYN-----PDAGYQQQYNPQGGYQQYNPQGG-----YQQQFNP
                                                                                                                                                                                                                                    Local Similarity 27.9 les 38; Conservative
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CITY: Lexington
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19911
                                                                                                                                                                                           6 QGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYY------
                                                                                                                                                         QAQPQQQQQQQQQQQQQA---PYQGHFQQSPQQQQQNVYFPLPPQSLTQPTSQSQQQQQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I: 542 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                      fractional yeast SSRP (fySSRP)
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Lippard, Stephen
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Pred. No. 0.092;
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RESULT 15
US-08-328-809-8
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                                                                                        Sequence 8, Application US/08328809 Patent No. 5705334 GENERAL INFORMATION:
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APPLICANT: Keilett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structu
TITLE OF INVENTION: Protein and
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NFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
 APPLICANT:
APPLICANT:
                                                      APPLICANT:
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ORIGINAL SOURCE:
ORGANISM: Sac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/539,906 FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,442
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                                                                                                                                                                                                                     123 SVTGTGASSNNNSNNN 138
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Local Similarity 27.9%;
nes 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                         63 QYANSNSNNNNVNVNALPQDFGYMQQTGSGQNYPTINQQQFSEFYNSFLSHLTQKQTNP 122
                                                                                                                                                                                                                                                                                                                            51 GYSGYQQGGYQQYN-----PDAGYQQQYNPQGGYQQYNPQGG---
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2 Militia Drive
Lippard, Stephen J.
Essigmann, John M.
Donahue, Brian A.
Toney, Jeffrey H.
Bruhn, Suzanne L.
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Protein and Uses
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; CLONE: fractional yeast SSRP (fySSRP) (predicted)
US-08-328-809-8
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Job time: 236 sec
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Best Local Similarity
Matches 38; Conserv
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APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Uses For DNA Structure-Specific TITLE OF INVENTION: Recognition Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                           123 SVTGTGASSNNNSNNN 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
                                                                                                                                                                                                                                                                                                                            95 Q-GGRGNYKNFNYNNN 109
                                                                                                                                                                                                                                                                                                                                                                63 QYANSNSNNNNVNVNVNALPQDFGYMQQTGSGQNYPTINQQQFSEFYNSFLSHLTQKQTNP 122
                                                                                                                                                                                                                                                                                                                                                                                                51 GYSGYQQGGYQQYN-----PDAGYQQQYNPQGGYQQYNPQGG-----YQQQFNP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid TOPOLOGY: linear
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Pred. No. 0.092;
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Maximum Match 100%
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Maximum DB seq
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A_Genesseq_1101:*
1: /SIDSB/gcgdatta
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length: 2000000000
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Copyright (c) 1993 - 2000
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N-PSDB; AAC86679.
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cancer	AAB58406	21	128		108.5
Amino acid sequenc	AAB30807	22	256		111
	AAG43593	21	1026	Ģ	111.5
Arabidopsis thalia	AAG43594	21	972	5	111.5
osis thali	AAG43595	21	946	5	111.5
icans	AAY95066	21	103	16.3	114
thal	AAG30909	21	324	6	115
thal	AAG30910	21	266		115
Arabidopsis thalia	AAG30911	21	171	16.4	115
dida albicans	AAY95064	21	103	16.4	115
	AAR27493	13	545	16.5	116
lworm	AAB83004	22	579	16.7	117
C	AAB83003	22	579	ა	117
thal	AAG29373	21	432	6.	18
thal	AAG29374	21	418	6	æ
	AAG29375	21	.398	6.	118.5
	AAG33721	21	1006	17.2	
	AAG33722	21	.994	17.2	
4	AAG33723	21	989		
	AAB48550	21	954		121
patriciarum	AAB35588	22	485		121
Ē	AAY27283	20	485		121
llimastix	AAW65462	19	485	17.3	121
21 human sec	AAB63197	21	280		· 121
NFAR-2	AAB35148	22	894		128
pMS10 contg. male	AAR06451	11	341		129
Nicotiana plumbagi	AAR75507	16	437	18.8	132
æ	AAW10628	18	341		134
	AAR09298	11	341		134
	8	11	341	٠	134
Tapetum-specific p	AAR06522	1	341	19.1	134
Amino acid sequenc	082	22	128	٠	135
Nicotiana alata ar	AAR75506	16	461	٠	136.5
Human chromosome-1	067	17	404	٠	141

## ALIGNMENTS

AB30792

D AAB30792;

C AAB30792;

X AAB30792;

X O2-APR-2001 (first entry)

X Manino acid sequence of a yeast Sup35 protein p

Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel

H

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XX
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XX
PT New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, PT also related aggregates, fibrils and polymers

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RESULT
AAB30800
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of a manner that creates a heritable change in phenotype. It is used to be a manner that creates a heritable change in phenotype.
                        N-PSDB;
                                     WPI; 2001-061723/07
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                                                                                                                                                                                                                                                                                                         amyloidogenic
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                                                                 Lindquist S,
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oldogenic domain; aggregation; fibril; phenotypic alteration;
therapy; disease resistance; plant pigmentation; prion disease
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                                                                  Sondheimer N,
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                                                                  Scheibel T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is used
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New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers -
                                                                                                                                                        Claim 11; Page 135-136; 188pp; English
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The present sequence represents a modified N region of Sup35 protein, in Ct the second oligopeptide repeat has been expanded twice, creating a total cof seven repeats. Sup35 possesses the prion-like capacity to undergo a cc self-perpetuating conformational alteration that changes the functional cstate of Sup35 in a manner that creates a heritable change in phenotype. It is used to construct chimeric polypeptides of the invention, which cc comprise at least one SCHAG (self-coalesces into higher-order aggregates) camino acid sequence fused in frame with a polypeptide of interest (which cc is other than a marker protein, a glutathione-S-transferase or a cc staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amylodogenic domain that causes capgregation into fibrils. The chimeric polypeptides are used to prepare cc polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable production, imparting disease resistance to plants, altering plant pigmentation and for Sequence 271 AA diagnosis and treatment of prion diseases

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Matches
                                            Query Match
Best Local
1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQ----
                                          Similarity
                                 Conservative
                                            97.3%;
87.2%;
                                0,:
                                          Score 682; DB 22; Pred. No. 2.1e-62;
                                 Mismatches
                                 0
                                                        Length 271;
                                 Indels
                                 18;
                                Gaps
          56
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                          103
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                         NENYNNNLQGYQAGFQPQSQG
nfnynnnlqgyqagfqpqsqg
                                                                                                  msdsnqgnnqqnyqqysqngnqqqgnnryqgyqaynaqaqpaggyyqnyqgysgyqqggy
                                               qqynpqggyqqynpqggyqqynpdagyqqqynpqggyqqynpqggyqqqfnpqggrgnyk
                                                                           -----QGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYK
                                                              123
                                                     120
                                                                           102
                                                                                                    60
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RESULT
AAB30799
                       AAB30799;
                                         AAB30799 standard; Protein; 215
                                                             w
(first entry)
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Sup35; phenotype; SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease

A modified N

region of yeast Sup35 protein

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Saccharomyces cerevisiae
                 Synthetic
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WO200075324-A2

14-DEC-2000

09-JUN-2000; 2000WO-US15876

PIN PRESENTATION OF THE PR 09-JUN-1999; 99US-0138833

(ARCH-) ARCH DEV CORP.

Lindquist S, Li L, Ma J, Liu ٦, Sondheimer z Scheibel H

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cc protein, in which four of the five oligopeptiue repeats the condergo a deleted. Sup35 possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of Sup35 in a manner that creates a heritable change in phenotype. CC It is used to construct chimeric polypeptides of the invention, which cc comprise at least one SCHAG (self-coalesces into higher-order aggregates) cC amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-5-transferase or a cC staphylococcal nuclear protein, a glutathione-5-transferase or a cC staphylococcal nuclear protein). The specification also describes considered the comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare cc specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein cc production, imparting disease resistance to plants, altering plant cc pigmentation and for diagnosis and treatment of prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAB30820
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                     SCHAG; self-coalesce; higher-order aggregate; amyloidogenic aggregation; fibril; phenotypic alteration; gene therapy;
                                                                                                                                                                                                                                                                                                02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                 AAB30820 standard; Protein; 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 133-134; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases also related aggregates, fibrils and polymers -
              09-JUN-1999;
                                                                                                                                                     Candida albicans
                                                                                                                                                                                      disease resistance; plant pigmentation; prion disease
                                                                                                                                                                                                                                                        Amino acid sequence of a Candia albicans protein.
                                               09-JUN-2000; 2000WO-US15876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSDSNOGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY 60
                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a modified N region of a yeast Sup35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                            (first entry)
              9908-0138833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.28;
69.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No. 1.1e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pqggrgnyknfnynnnlggyqagfgpq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                          domain;
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AAB30810
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Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes chimeric polypeptides which comprise at cleast one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-5-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion datased related aggregates, fibrils and polymers.
                                                                                                                                                                                                                    SCHAG; self-coalesce; higher-order aggregate; amyloidogenic aggregation; fibril; phenotypic alteration; gene therapy;
                                                                                                                                                                                                                                                                                                  02-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  AAB30810 standard; Protein; 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                           09-JUN-2000;
                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                   Amino acid sequence of a prion-like amyloidogenic protein.
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                                              09-JUN-1999;
                                                                                                                                          WO200075324-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQQ-GGYQQYNP-DAGYQQQYNPQGGYQQ-YNPQGGYQQQFNPQGGRGNYKNFNYNNNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       manaslngdqskqqqqqqqqqqqqqqn-----yynpnaaqstvpqqgqqqqqqqqqqq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQ-;--PAGGY--YQNYQGYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                      resistance; plant pigmentation; prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   715 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                             2000WO-US15876
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                                              99US-0138833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.5%; Score 228; DB 22;
43.2%; Pred. No. 3.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sondheimer N,
                                                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scheibel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                        domain;
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(ARCH-) ARCH DEV CORP

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AAB30821
ID AAB3
XX AAB3
XX AAB3
XX AAB3
XX AGA
DT 02-J
XX AGA
KW SCHJ
KW AG9U
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Best Local
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                                                                                                                     09-JUN-1999;
                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                                                                  14-DEC-2000
                                                                                                                                                                                                                                                                                      WO200075324-A2
                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                            aggregation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-2001
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        Lindquist S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a putative prion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB30821 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                               (ARCH-) ARCH DEV CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 smaqsylgggqtqsn----qqqynqqgqnnqqqqqqqqqqqqqqqqqqq---qghss
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                                                                                                                                                                                                                                                                                                                                                                                                   resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405
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                                                                                                                                                                            2000WO-US15876
     Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                       fibril;
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                                                                                                                                                                                                                                                                                                                                                                                          phenotypic alteration; gene therapy;
plant pigmentation; prion disease.
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Pred. No. 3.7e-09;
7; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405
     Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu
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     Sondheimer N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sondheimer N,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                              SCHAG; self-coalesce; higher-order aggregate; amyloidogenic aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease.
                 Lindquist S,
                                                                                 09-JUN-1999;
                                                                                                                 09-JUN-2000; 2000WO-US15876
                                                                                                                                                  14-DEC-2000
                                                                                                                                                                                  WO200075324-A2
                                                                                                                                                                                                                 Pichia
                                                                                                                                                                                                                                                                                                              Amino acid sequence of a Pichia pinus protein
                                                                                                                                                                                                                                                                                                                                                02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                               AAB30819;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAB30819 standard; Protein; 741 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 182-183; 188pp; English.
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                                                 (ARCH-) ARCH DEV CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 sfsalasmassylgnnsnsnssyggqqqaneyg-rpqhng
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55; Conserv
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                 Li L,
                                                                                   99US-0138833
                  Ma
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                  Liu
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Pred. No. 3.7e-09;
7; Mismatches 44;
                  ٦,
                  Sondheimer N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 405;
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                    Scheibel
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
Claim 5; Fig 4; 51pp; English
                             regulatable
                                             controlled
                                                                                                                                   Fink GR,
                                                                                                                                                                                                                           23-JUN-1988;
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                                                                                                                                                                                                                                                                                                                    Saccharomyces
                                                                                                                                                                                                                                                                                                                                               Yeast promoter; yeast pheromones; FUS-1; BIK-1; HIS-4
                                                                                                                                                                                                                                                                                                                                                                             ORF incorporated within the HIS4 gene
                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1990
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                                                                                                                                                                 (WHIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 QNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                        DNA fragment contg. protein encoding gene and yeast promoter trolled by mating pheromone allowing efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid encoding chimeric proteins with self-assembly perties, useful e.g. for diagnosis and treatment of prion do related aggregates, fibrils and polymers -
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45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                    cerevisiae
                                                                                                                                                                                             87US-0066078
                                                                                                                                                                                                                           88WO-US02129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
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Pred. No. 7.9e-09;
7; Mismatches 36
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Best Local
                   21-APR 1999
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04-MAY 1999
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06-MAY 1999
06-MAY 1999
07-MAY 1999
                                                                                                                                              08-APR-1999;
16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                 09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORF lies between the FUS 1 or BIK 1 promoter, BIK 1 running 3' to At least one polypeptide may be promoted within a high-copy vector induced by a-factor for alpha cells, alpha-factor for a-cells usin
                                                                                                                                                                              01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                           25-FEB-2000;
                                                                                                                                                                                                                                                                                                                    EP1033405-A2
                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG30013 standard;
                                                                                                                                                                                                                                                                                                                                                            termination sequence.
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                                                                                                                                                                                                                                                                           2000EP-0301439
99US-0132485.
99US-0132486.
99US-0132486.
99US-0132863.
99US-0134256.
99US-0134218.
99US-0134219.
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99US-0130510.
99US-0130891.
99US-0131449.
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99US-0127462.
99US-0128234.
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99US-0132407.
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99US-0125788
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Pred. No. 1.6e-08;
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Best Local S
Matches 57
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   06-SEP-2000
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R 21-0CT-1999; R 21-0CT-1999; R 21-0CT-1999; R 22-0CT-1999;	R 21-OCT-1999; R 21-OCT-1999;	R 18-OCT-1999; R 21-OCT-1999;	R 14-0CT-1999; R 14-0CT-1999;	R 14-OCT-1999; R 14-OCT-1999;	R 13-OCT-1999;	R 13-OCT-1999; R 13-OCT-1999;	08-OCT-1999; 12-OCT-1999;	07-0CT-1999;	05-OCT-1999;	29-SEP-1999; 04-OCT-1999;	24-SEP-1999; 28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999;	13-SEP-1999;	07-SEP-1999;	R 31-AUG-1999; R 31-AUG-1999;	R 27-AUG-1999;	R 27-AUG-1999;	R 25-AUG-1999;	R 23-AUG-1999;	R 20-AUG-1999;	R 18-AUG-1999; 9	R 17-AUG-1999;	R 13-AUG-1999;	1999;	1,6661	AUG-1999;	R 06-AUG-1999;	R 06-AUG-1999;	R 05-AUG-1999; 9	R 04-AUG-1999; S	R 03-AUG-1999;	R 02-AUG-1999; ;	R 28-JUL-1999; 9 R 02-AUG-1999; 9	R 27-JUL-1999; 9 R 27-JUL-1999; 9	R 26-JUL-1999; 9 R 27-JUL-1999; 9
R 21-OCT-1999; 99US R 21-OCT-1999; 99US R 21-OCT-1999; 99US R 22-OCT-1999; 99US	R 21-OCT-1999; 99US R 21-OCT-1999; 99US	R 18-OCT-1999; 99US R 21-OCT-1999; 99US	R 14-OCT-1999; 990S R 14-OCT-1999; 990S	R 14-0CT-1999; 990S R 14-0CT-1999; 990S	R 13-OCT-1999; 99US	R 13-OCT-1999; 99US R 13-OCT-1999; 99US	08-OCT-1999; 99US 12-OCT-1999; 99US	07-0CT-1999; 99US	05-OCT-1999; 99US	29-SEP-1999; 99US 04-OCT-1999; 99US	24-SEP-1999; 99US	23-SEP-1999; 99US	20-SEP-1999; 99US	15-SEP-1999; 99US	13-SEP-1999; 99US	07-SEP-1999; 99US	R 31-AUG-1999; 99US R 31-AUG-1999; 99US	R 27-AUG-1999; 99US	R 27-AUG-1999; 99US	R 25-AUG-1999; 99US	R 23-AUG-1999; 99US	R 20-AUG-1999; 99US R 20-AUG-1999; 99US	R 18-AUG-1999; 99US R 20-AUG-1999; 99US	R 17-AUG-1999; 99US	R 13-AUG-1999; 99US	1999; 99US 1999; 99US	S066 (6661	AUG-1999; 99US	R 06-AUG-1999; 99US:	R 06-AUG-1999; 99US	R 05-AUG-1999; 99US	R 04-AUG-1999; 99US-	R 03-AUG-1999; 99US-	R 02-AUG-1999; 99US: R 02-AUG-1999; 99US-	R 28-JUL-1999; 99US- R 02-AUG-1999; 99US-	R 27-JUL-1999; 99US- R 27-JUL-1999; 99US-	R 26-JUL-1999; 99US- R 27-JUL-1999; 99US-
PR 21-OCT-1999; 99US-0160704 PR 21-OCT-1999; 99US-0160814 PR 21-OCT-1999; 99US-0160815 PR 22-OCT-1999; 99US-0160815	R 21-OCT-1999; 99US-016 R 21-OCT-1999; 99US-016	R 18-OCT-1999; 99US-015 R 21-OCT-1999; 99US-016	R 14-0CT-1999; 99US-015 R 14-0CT-1999; 99US-015	R 14-OCT-1999; 99US-015 R 14-OCT-1999; 99US-015	R 13-OCT-1999; 99US-015	R 13-OCT-1999; 99US-015 R 13-OCT-1999; 99US-015	08-OCT-1999; 99US-015 12-OCT-1999; 99US-015	07-0CT-1999; 99US-015	05-0CT-1999; 99US-015	29-SEP-1999; 99US-015	28-SEP-1999; 990S-015	23-SEP-1999; 99US-015	20-SEP-1999; 99US-015	15-SEP-1999; 99US-015	13-SEP-1999; 99US-015	07-SEP-1999; 99US-015	R 31-AUG-1999; 99US-015 R 31-AUG-1999; 99US-015	R 27-AUG-1999; 99US-015	R 27-AUG-1999; 99US-015	R 25-AUG-1999; 99US-015	R 23-AUG-1999; 99US-014	R 20-AUG-1999; 99US-014	R 18-AUG-1999; 99US-014 R 20-AUG-1999; 99US-014	R 17-AUG-1999; 99US-014	R 13-AUG-1999; 99US-014	1999; 99US-0141 1999: 99US-0141	1999; 99US-0141	AUG-1999; 99US-014	R	R 06-AUG-1999; 99US-014	R 05-AUG-1999; 99US-014	R 04-AUG-1999; 99US-014:	R 03-AUG-1999; 99US-014	R 02-AUG-1999; 99US-0140 R 02-AUG-1999; 99US-0140	R 28-JUL-1999; 99US-014: R 02-AUG-1999; 99US-014:	R 27-JUL-1999; 99US-014: R 27-JUL-1999; 99US-014:	R 26-JUL-1999; 99US-014! R 27-JUL-1999; 99US-014!

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Best Local Similarity 34.8
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999
25-OCT-1999
25-OCT-1999
25-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
29-OCT-1999
                                                                                                          Peptide
            19-JUL-1994;
                                                       01-FEB-1996
                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                  HOMO
                                                                                                                                                                                                                                                                                                                    tyrosine phosphorylation site; phosphatidylinositol-3-kinase; Xp11.2; SYT-SSX1; SYT-SSX2; fusion protein; primer; PCR; polymerase chain reaction; probe; antibody; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                     Human; SYT; synovial sarcoma; translocation; chromosome-18;
18q11.2; X-chromosome; SSX1; SSX2; gene fusion; SH2; SH3; Grb2;
                                 19-JUL-1995;
                                                                             W09602641-A2
                                                                                                                                  Domain
                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                               humanised antibody; hybridisation; antisense; antitumour; recombinant vaccine; vaccinia virus; vector; cancer; diac
                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR90675 standard; Protein;
                                                                                                                                                        Domain
                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                             Кeу
                                                                                                                                                                                                                                                                                        therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR90675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 nynpqga-gnfgpasgagnlgpapgagnpgygqgysgpgqeqnq 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 QNYQQYSQNGNQ---QQGNNRY---QGY----QAYNAQAQP--AGGYYQN-----YQG 51
                                                                                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSGYQQG------GYQQYN------PDAGYQQQYNPQGGYQQYN----PQGGYQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qnfqrntqygqqppmqgggsygpqqgyatpgqggtqapppfqggynqgprsppppyg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFNPQGGRGNYKNFNYNNNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -agynqgqgspvppyqagynqvqgspvppyqgtqssyg-qggsgnysqgppggynqggpr 351
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0161404
99US-0161405
99US-0161406
99US-0161359
99US-0161360
99US-0161361
99US-0161902
99US-0161992
99US-0161993
99US-01621442
            94GB-0014580
                                 95WO-GB01704
                                                                                                                                                       /note= "(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0160989
                                                                                                             /note= "(
                                                                                                                                                                                                            /note=
67..70
                                                                                                                                                                                                                                  Location/Qualifiers 67
                                                                                                                                  399..402
                                                                                                                                                                             362..365
                                                                                                                                                                                      /note= "Phosphatidylinositol-3-kinase SH2 binding
domain"
                                                                                                                                                                                                                                                                                                                                                                                    SYT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.1%;
                                                                                                                      "Grb2 SH2 binding domain
                                                                                                                                         "SH3 binding domain
                                                                                                                                                                "Grb2 SH2 binding domain'
                                                                                                                                                                                                                       "Tyrosine phosphorylation site"
                                                                                                "Peptide removed by SSX2 rearrangement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148; DB 21;
Pred. No. 2.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QGYQAGFQPQSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                               cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is encoded by the SYT gene (synovial sarcoma ctranslocation). The gene is at the location of a chromosome-18q11.2 Cb breakpoint associated with synovial sarcoma, and is associated with CC the translocation t(x;18)(p11.2;q11.2) found in human synovial certains and involving joining of the SYT gene to either SSX1 (encoding AAR90676) or SSX2 (encoding AAR90677) on the x-chromosome at CC (encoding AAR90676) or SSX2 (encoding AAR90677) on the x-chromosome at CC (AAR90679) or SYT-SSX2 (AAR90678) fusion proteins. The SYT protein is CC (AAR90679) or SYT-SSX2 (AAR90678) fusion proteins. The SYT protein is CC rich in glutamine (19%), proline (16%) and glycine (14%), and there CC are several consensus glycosylation and phosphorylation sites. CC Detection of the gene or its product either in an abnormal location CC or as a fusion may be used in diagnosis of synovial sarcoma, using CC primers, probes, humanised antibodies, monoclonal antibodies, etc. CC Antisense oligonucleotides and antibodies may also be used therapeutically, and antitumour recombinant vaccines may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing synovial sarcoma by detection of e.g. SYT and SSX1 sequences, based on X18 trans-location - by amplification of trans-location sequences or detection of the encoded protein
Misc-difference
                                                                                                                                                                                                                                                                                                                                   AAR75506 standard; Protein; 461
                              Misc-difference
                                                             Peptide
                                                                                                                                                Nicotiana
                                                                                                                                                                                                Arabinogalactan
                                                                                                                                                                                                                                 Nicotiana alata arabinogalactan protein NaAGP1 encoded by cDNA
                                                                                                                                                                                                                                                                  05-DEC-1995
                                                                                                                                                                                                                                                                                                  AAR75506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6;
                                                                                              Peptide
                                                                                                                                                                                 adhesive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooper CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                                                                                                                                                 366 pgg---ggqqyggyrptqpg 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mgqvnqgnhmmgqrqippyrppqqgppqqysgqedyygdqyshggqgppegmnqqyypdg 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYNNNLOGYQ-AGFQPQSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nsqygqqddayqgpppqqgyppqqqqypgqqyp-----gqqqgygpsqggppqypny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSDSNQGNNQQNYQQY-----SQNGNQQQ--GNNRYQGYQ-AYNAQAQPAG----GYYQNY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGYSGYQQGGYQQYNPDAGY---QQQYNPQGGYQQYNPQGGYQQQFNP-QGGRG-NYKNF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 4a;
                                                                                                                                                  alata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                (first entry)
/note= "Ala in peptide" 37
                             /note= "corresp. to microsequenced peptide"
26
                                                                                                                                                                                                protein;
                                                                                                               Location/Qualifiers
                                                                               /label- signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%;
                                                                                                                                                                                                  AGP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 17;
Pred. No. 1.4e-06;
9; Mismatches 55;
                                                                                                                                                                                                gum; thickening agent; emulsifier,
                                                                                                                                                                                                                                                                                                                                   ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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RESULT 14
AAB30822
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                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                     plumbaginafolia. Degenerate reverse primers corresponded to AGP N-terminal AA sequence were synthesised and used to obtain a company of the primer extension product, which was then amplified by PCR. Additional primers, corresp. In sequence to parts of the 160-bp of fragment were synthesised and used to amplify the 3' part of the AGP gene by nested PCR. The primers were AAQ92536 and AAQ92537. A company of the PCR. The primers were AAQ92536 and AAQ92537. A company of the two PCR reactions gave rise to a DNA sequences obtd. From the two PCR reactions gave rise to a DNA sequence shown. The PCR fragment encodes a protein contq. The PCR fragment was used to screen a cDNA company made from RNA isolated from N. alata cells. The alignment of the PCR sequences with the cDNA sequence gave rise to AAQ92524. The calc. mol. wt. of the encoded protein is 51.8 kD with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The N-terminal region of an arabinogalactan protein (AGP) was obtd from N. alata suspension culture. It was used as a template for the synthesis of an oligo primer which was further utilised for the isolation of a hybridising AGP gene from both N. alata and N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1994;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant plant arabinogalactan protein and cloned DNA encoding it useful as an emulsifying agent, adhesive agent or a lubricating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-215258/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALBR ) ALBRIGHT & WILSON AUSTRALIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                              Sequence
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                                                         300 synnn 304
                                                                                                                        240
                                                                                                                                                                                     181
                                                                                         106 -YNNN 109
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                      54
                                                                                                                                                                                                                 3 DSNOGNNOONYQOYSONGNOOGG---NNRYQGYQAYNAQAQPAGGYYQNY-----QGYS- 53
                                                                                                                     nynngysqsynnnnnfysenynnnnnnvfsensnnngyskkinnngysqnymnnnngfse
                                                                                                                                                    GYQQGGYQQXNPDAG-YQQQYNPQGG--YQQYNPQGGYQQQFNPQGGRGNYKNFN----- 105
                                                                                                                                                                                  dsnnndnnngydsnnnnnnnddgfsenynnngy-senannknnngysenynnnnnngyak 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Figure 1F; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                            pI of 3.84.
                                                                                                                                                                                                                                                                                                                              461 AA;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0276452
93US-0161944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "microsequenced derived SEQs identical" 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "X in peptide" 26..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "microsequenced and derived SEQ identical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note- "microsequenced and derived SQ identical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clarke AE,
                                                                                                                                                                                                                                                                19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "His in peptide"
                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                Score 136.5; DB 1
Pred. No. 4.7e-06;
3; Mismatches 54
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RESULT 15
AAR06522
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                                                                                                                                                                                                                                                                                                                                                                              identified from a yeast protein database. The specification describes chimeric polypeptides, which comprise at least one SCHAG (self-coalesces into higher-order aggregates) aminol acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease cresistance to plants, altering plant pigmentation and for diagnosis
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers -
 03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy;
                               AAR06522;
                                                           AAR06522 standard;
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB30821-23 represent putative prion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 183-184; 188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-1999;
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                                                                                                                                      66 gynqqgynq----qgynqqgynqqgynqqghqqpvyvqqqppq--rgn 107
                                                                                                                                                            54 GYQQGGYQQYNPDAGYQQQ-YNPQGGYQQYNPQQGYQQQFNPQGGRGN 100
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                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                     h 19.3%;
Similarity 40.7%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                     128 AA;
(first
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                                                           protein;
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Pred. No. 1.4e-06
4; Mismatches 3
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Search completed: February 1, Job time: 254 sec
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                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the promoter is used in a gene construct with a distructer gene such as the mammalian uncoupling protein gene, or a mutated form of the gene for the beta subunit of F1-AFDase. The promoter operates in the target tissue and expression of the distributer gene inhibits respiration resulting in cell death. This is of particular use for inhibiting male fertility in maize crops where cell death results in failure to produce viable pollen. When inserted into a gene cascade, as a module which permits external control of expression, fertility may also be restored if required. See also AAR06524 and AAR06525.
                                                                                                                                                                                                                                                                                                                                                        Sequence
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N-PSDB; AAQ05759.
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                                                                       237 nnpqertnfsqgqgggfrp 255
                                                                                                                                                                                                   126 srpsrtdrnrnyrgnyqdgppqqgn----yq--nnrpppeggyqnnppqqgnyqtyrsq 178
                                                                                                         102 KNFNYNNL-QGYQAGFQP 119
                                                                                                                                                           56 QQGGYQQYNPDAGYQQ-------QYNPQGGYQ---QYNPQGGYQQQFNPQGGRGNY 101
                                                                                                                                                                                                                         2 SDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQ-----NYQGYSGY 55
                                                                                                                                       qdg--rgyapqqnyaqggqdgrgfgrndytdrsgyngptdfrsqtqyqghvnpagqgqgy 236
                                                                                                                                                                                                                                                                                                                                                        341 AA;
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               2002, 15:01:49
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044011 dictyosteli
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02189 caenorhabdi
042451 triticum ae
09sdm3 triticum ae
041516 triticum ae
041679 plasmodium
076853 dictyosteli
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Q20497 caenorhabdi
Q19662 caenorhabdi
Q19414 caenorhabdi
Q9ve19 drosophila
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MEDLINE-87286864; PubMed-3302672;

Trueheart J. Boeke J.D., Fink G.R.;

"Two genes required for cell fusion during
for a pheromone-induced surface protein.";

Mol. Cell. Biol. 7,2316-2328(1987).

EMBL; M16717; AAA34615.1; -.
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ENTS	Q21163 caenorhabdi Q9ydri drosophila Q9gcz dictyosteli Q41725 zinnia eleg Q9yvs8 drosophila Q9yy0 triticum ae Q9y101 dictyosteli Q9yy19 drosophila Q1334 homo sapien Q9zix4 mus musculu Q41256 nicotiana a Q96902 dictyosteli Q21073 caenorhabdi Q40054 hordeum vul Q49545 yarrowia li Q38767 aegilops ta Q40045 hordeum vul Q9w4f1 drosophila Q9w4f1 drosophila Q9w4f1 drosophila Q43117 colletotric Q9jil3 rattus norv Q75177 homo sapien Q24588 drosophila Q9vz20 drosophila Q9vz20 drosophila Q9vz20 drosophila	_

## O94079 PRELIMINARY; PRT; 407 AA. O94079; O1-MAY-1999 (TrEMBLrel. 10, Created) O1-MAY-1999 (TrEMBLrel. 10, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) YEAST (S. CERENCHE) FUSI (FUSION GENE) AND BIKI Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomyces. NCBI\_TaxID=4932; AND YCL028W. update) BIK1 GENE REGION Saccharomycetes;

yeast

conjugation: evidence

SQ DR	SEQUENCE 407 AA; 43262 MW; 6B26940F74A804C3 CRC64;
- P	Query Match 66.4%; Score 895; DB 3; Length 407;
ма	Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy	1 QGQGQGQGQGQGQGQGQGGGGTALASSASSAMUSUNUNQQGQNQSSGGSSFGALASMAS 60
Db	153 QGQGQGQGQGQGQGQGQGGFTALASLTSSFMNSNNNNQQGQNQSSGGSSFGALASMAS 212
Qy	61 SEMHSNNNNONSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGGAFSSLAS 120
Db	213 SFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLAS 272
Qy	121 MAQSYLGGGQTQSNQQQYNQQGQNNQQQQQQQQGQNYQHQQQGQQQQQGHS 170
Db	273 MAQSYLGGGQTQSNQQQYNQQGQNNQQQQQQQNYQHQQQGQQQQQGHS 322

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Q1-JUN-1998
Q1-JUN-2001
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Wathstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                            Q19662
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InterPro; IPR000561; EGF-11ke.
PROSITE: PS00022; EGE_1; UNKNOWN_1.
PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 3498 AA; 400778 MW; 283FFC65A6B9E336 CRC64;
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EMBL; Z49888; CAA90064.1; -.
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                                                                                                                                                                                                                                                         SSNASSQQGGSSQMQQSGYGMPGNQMQMQQNQKQQVQRGMPTGMGQTNMGQSGMGQSGMG
                                                                                                                                                                                                                                                                                           NSNSNSSYGG--QQQANEYGRPQHNGQQQSNEYGRPQYG------GNQNSNGQHES---
                                                                                                                                                                                                                                                                                                                                                       TAPQQAQNPQASQSY-GQQQTQQNRYGMGSSGYTANSGGSSNILNQSMEESGLNQGFSGA
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Caenorhabditis.
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                            PRT;
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Best Local :
Q19414
Q19414;
01-NOV-1996
01-NOV-1996
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SEQUENCE 382 AA; 42877 MW.
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Bonfield J., Burton J., Connell M., Copsey T., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
elegans.";
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1998 (TrEMBLrel. 08, Last annotation
SIMILARITY TO E. COLI CELL DIVISION PROTEIN
F21C10.8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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Du Z., Gattung S.;
Submitted (APR-1996)
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                                                                                                                 ANQNGQYQNTQYQQQNGQNGQNQF---QQSNGQNQNSQYQQTSNQQMNN
                                                                                                                                 ANEYGRPQHNG-QQQSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNN
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                                                                                                                                                                                                                                                                                          QQGQQNNYGTQAQYDAGQNQMGQSGQVQGYSNNGYSNQNSQMSQSQASSG---SSSVSLM 169
                                                                                                                                                                                                                                                                                                                     QQGYNQSY----QNGNQNS-----QGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMA
                                                                                                                                                                                                                                                                                                                                                QNQQYGS-----NNQQNQNQNQNQQNSNQYSTTSNM------NNQQNSNQY 112
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                                           PRELIMINARY;
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Last annotation update)

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Best Local
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Q1-MAY-2000 (TrEMBLrel. 1)
Q1-MAY-2000 (TrEMBLrel. 1)
Q1-JUN-2001 (TrEMBLrel. 1)
CG4090 PROTEIN.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z6938; CAA93412.1; -. InterPro; IPR003677; DUF148. Pfam; PF02520; DUF148; 1. SEQUENCE 409 AA; 43231 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-94150718; PubMed-7906398;
   Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Trac
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                                                                                                                                                                                                                                    QYGGNQNSNGQHESFNFSGNFSQQNNNGNQNRY 253
                                                                                                                                                                                                                                                             DIINNLATVQASIEGIQSNTSSSENDRQSAFQALQQAHPMEYSVLTSLQNQHEQTQYAR-
                                                                                                                                                                                                       -MGSNGNSNSNYGNSNFNSNYGNNGYNHNGNNY 388
                                                                                                                                                                                                                                                                                              SSFSALASMASSYLGNNSNSSYGGQQ---QANEYGRPQH----NGQQQSNEYGRP 220
                                                                                                                                                                                                                                                                                                                              NVSSSAAQDYYNIVNNKSLTTNQINEQASNWASANSVQAQYIQYETNRSAIHTQATQNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGYGQNQGSMQGYSQQGYGGNSQQDYGYSQSQGSGMGVQGYGGS---SQSYGQQAFAQQQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43231 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                            -----NQQGQNNQQQYQQQGQNYQHQQQGQ----QQQQGHS 170
                                                              13,
13,
17,
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                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 232;
Pred. No. 5
                                                                                             Created)
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B07DF0E4175C5739 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
Tracheata; Hexapoda; Insecta;
                                                                                                                           2112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ballew R.M., Basu A., Baxendale J., Bayraktaróglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.H., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I. Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann V. Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Well M.; HI., Ibegwam C., Jalali M. Kallush F. Karnen G. H. Ker Z., Kentison J. A. Ketchum K. J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00022; EGF_1; 1. SEQUENCE 2112 AA; 219547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF01607; Chitin_bind_2;
SMART; SM00494; ChtBD2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002557; Chitin_binding
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0038492; CG4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                   443
112 GGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHSS
                                                            503
                                                                                                                                                                                                                                                                                                         383
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                                                                                                                                                                                                                                                                                                         GSNQSSGNNQSSSSNQSSSNQSSNNNQSSSSNSNQTSSSSQNNSGSNKPVPTECEDENT 442
                                                                                                                                                                                                                                                                                                                                                                      GQGQGQGQGQGQGQGQGSFTALASLASSFMNSNNNNQQGQNQS-----
                                                            SGSNNSGQQSSGSSSNNQGSSNNQSSSNQS----SSNNQGSSNNQGSSSNQGSSSNQGSS
                                                                                                                      FGALASMASSEMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQS 111
                                                                                                                                                                                   YIPDKEDCAKFYRCRQDKDGKLEQVPFTCGPGTVWNQVDKVCDLPTEDQKKKCNIQSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 226.5; DI
Pred. No. 8.1e-1
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B91018E5551A5D36 CRC64;
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Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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      171
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Best Local S
Matches 89
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                                                                     O9DEY1 PRELIMINARY; PRT; 421 AA.

O9DEY1;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OVARIAN FIBROIN-LIKE SUBSTANCE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Fukuzawa M., Araki T., Adrian I., Williams J.G.;

*A Dictyostelium STAT protein that is activated by the stalk inducer DIF regulates multiple developmental events.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ301670; CAC33514.1; -.

SEQUENCE 929 AA; 106988 MW; ADC15D743C18D233 CRC64;
                     Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSTC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATC PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                             212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AQIQQQQAQQIQQQQAQIQAQQAQIQQQQLEQQHLQQQQFQFQQQQ--QQQQQQQQQQQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 225.5; DB 5; Pred. No. 4.6e-12;
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                        Vertebrata; Euteleostomi;
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Best Local
                                                                    Pfam; Pf00046; homeobox; 1.
PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
SMART; SM00389; HOX; 1.
                                                                                                                                                                     Development 0:0-0(1998).

EMBL; AF036171; AAB92246.1; -.

InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mycetozoa; NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (Tremblrel. 06, 01-JUN-1998 (Tremblrel. 06, 01-JUN-2001 (Tremblrel. 17, HOMEOBOX-CONTAINING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substance to fertilization enve
Submitted (SEP-2000) to the EMEL; AF309411; ARG25716.1; -.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
SEQUENCE
                          NON_TER
                                               Homeobox; DNA-binding; Nuclear
                                                                                                                                                                                                                                                    Han Z., Firtel R.A.
                                                                                                                                                                                                                                                                              STRAIN-KAX3;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SMACY217; WAF; 1.
SMOO217; WAF; 1.
PROSTITE; PS00317; 4_DISULFIDE_CORE; 1.
SEQUENCE 421 AA; 38510 MW; 99698CF275C6FED7 CRC64;
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"Transglutaminase activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GYQQQQGQSGGAFSSLASMAQSY-LGGGQTQSNQQQYNQQGQNNQQQYQQ---QGQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGAGQGAGQGSGYGQGSGYGQGSGQGAGQGSGYGQGSGYGQGSGYGQGSGQGAGQGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGQGSGQGAGQGSGYGQGAGQGSGY-----GQGSGYGQGAGQGSGYGQGSGYGQGA
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534 AA;
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62310 MW;
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Dictyostellida;
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envelope for adhes:
e EMBL/GenBank/DDBJ
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Pred. No. 3e-12;
.2; Mismatches 144;
                                                                                                                        UNKNOWN_1
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01326F3DD65FCFA8
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CRC64;
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11;

Best Local Similarity

16.5%; 23.3%;

Score Pred.

No. 5.

DB 5; .6e-12;

Length

Query Match

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В

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Query Match
Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL022245; CAA18304.1; EMBL; AL031764; CAA21105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
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01-AUG-1998 (TrEMBLrel. 16, Last sequence update)
01-AUG-1998 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation 2320.02C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               059779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 468-658 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             V., Rajandream M.A., Barrell B.G., Murphy L.,
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                                                                                                                                                          SSFM-HSNNNQNSNNSQQGYNQSYQNGNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSL 118
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                                MASSYLGNNSNSNSSYGGQQQ 199
                                                                QGLASSFLNSSSGNSNKQNYN--NNNNQNYGNNNNQNY-
                                                                                                                                   SSFLGSSGNNNNNNNSG-----NYNNNNSGNNNQQHQ----
                                                                                                                                                                                                     QGSSGGLSAAAVSGLIGSFMGSSSNNSNSSNNNSNTSNNNSNTSNNESMVSKLSSLSGMA 553
                                                                                                                                                                                                                                       QGQGQG-SFTALASLASSFM-----
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                                                                                                ASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHSSSFSALAS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNNNSNNRGKNFSDSGS-----SDSDSELNRHNNNNNNNS-NNYNNGNSNSNNNRNNNN 311
                                                                                                                                                                                                                                                                                                                                                           658 AA; (
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-NNNNNSSQGGNSQ 642
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Pred.
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                                                                                                                                                                                                                                                                                       222; DB 3;
No. 6.8e-12;
                                                                                                                                                                                                                                     ---NSNNNNQQGQNQSSGGSSFGALASMA 59
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Q03871
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044011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theor. Appl. Genet. 75:11/-126(195/).

1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSSPERM.

1- MISCELLANEOUS: THESE PROTEINS OCCUR AS DISULFIDE-BRIDGE LINKED AGGREGATES, AND ARE THOUGH TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEATH DOUGH.

PROPERTY OF WHEATH DOUGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 1BY9 PRECURSOR
044011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQQPGQGQGYYPTS.

EMBL; X61076; CAA43361.1; -.

PIR; S18733; S18733.

Mendel; 14737; Triae; 2380; 14737.

InterPro; IPR001768; Cereal_tryp_amyl_inh.

InterPro; IPR001419; Glutenin.

Pfam; PF00234; tryp_alpha_amyl; 1.

PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLU-IBY9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halford N.G., Forde J., Anderson O.D., Greene Theor. Appl. Genet. 75:117-126(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- miscellaneous: the mature protein is characterized by a large number of well preserved repeats of the two motifs: gaapeg an
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                                                                                   419
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                                                                                                                 YGRPQHNGQQQSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGNQNRY
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                                                                                 LGQRQQPGQGQQTRQGQQLEQGQQPGQGQQTRQGQQLEQGQQPGQGQQGYY 469
                                                                                                                                                   SQQQPGQGQQRHYPASLQQPGQGQQGHYT--ASLQQPGQGQQGHYPASLQQVGQGQQIGQ
                                                                                                                                                                                     --QQQGQNYQHQ-----QQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANE
                                                                                                                                                                                                                     SQQQPGQGQYPASQQQPGQGQQGQYPASQQQPGQGQQGQYPASQQQPGQGQQGHYLA
                                                                                                                                                                                                                                                                                       GQQLGQGRQI-----GQGQQSGQGQQGYYPTSPQQLGQGQQPGQWQQSGQGQQGYYPT
                                                                                                                                                                                                                                                                                                                         GSSFGALASMASSFMHSNNNQNSNNSQQGYNQS----
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PRELIMINARY;
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28.9%; Pred
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PRT;
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No. 7.3e-1
1457
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R Pfam; PF00069; pkinase; 2.

R SMART; SM00220; S_TKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

JR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Serine/threonine-protein kinase; Tr:

ATP-binding; Serine-protein kinase; Tr:

ATP-binding; 
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Best Loc
Matches
                  01-NOV-1996
                                                                Q41553
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASE:
EMBL; AF045453; AAC02554.1;
HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96042901; PubMed-8536963; Loomis W.F., Welker D., Hughes J., N"Integrated maps of the chromosomes Genetics 141:147-157(1995).
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                           Q41553;
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InterPro; IPR002290; Ser_thr_kin_actsite
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Proc. Natl. Acad. Sci. U.S.A. 93:5562-5566(1996).
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Kuspa A., Loomis W.F
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Local Similarity
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                                                                                                                                                                          KQQQKNLHHQQQQQQRFMQVGSP 1046
                                                                                                                                                                                                                                                                                            NOQQYQQQQQNYQHQQQQQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQ-QANEY
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                    (TrEMBLrel.
                                                              PRELIMINARY;
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Pred. No. 2.9e
25; Mismatches
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s in Dictyostelium discoideum.
                                                              815
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2.9e-11;
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Matches 87
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STRAIN=CV. Check
Forson O.D.,
SEQUENCE FROM N.A.
STRAIN-CV. HOPE; TISSUE-ENDOSPERM;
Halford N.G., Field J.M., Blair H.,
                                                                                                                        Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
Triticeae; Triticum.
                                                                                                                                                                                                                                   01-NOV-1996 (TYEMBLIEL. 01, Created)
01-NOV-1996 (TYEMBLIEL. 01, Last sequence update)
01-UN-2001 (TYEMBLIEL. 17, Last annotation update)
HIGH MOLECULAR WEIGHT GLUTENIN SUBUNIT 1AX1 PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; F
SEQUENCE
                                                                                                                                                                                                                   GLU-1AX1
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                                                                                                                                                                                       Triticum aestivum (Wheat)
                                                                                                                                                                                                                                                                                                                                003872;
                                                                                                                                                                                                                                                                                                                                                     Q03872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation TRICTICUM AESTIVUM HIGH MW GLUTENIN SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson O.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. CHEYENNE;
Anderson O.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQ-QQSNEYGRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQ-GQNNQQQYQQQGQNYQHQQQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QQSGQGQQLGQGQQGQQPGQKQQSG-QGQQGYYPISPQQLGQGQQSGQGQLGYYPTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFMHSNNNQNSNNSQQGY--NQSYQNGNQNSQGYN-----NQQYQGGNG--GY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQSGQGQSGYYPTSAQQPGQLQQSTQEQQLGQEQQDQQSGQG--RQGQQSGQRQQDQQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; Conserv
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.D., Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            815 AA;
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                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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A; 88476 MW;
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                                                                                                                                           Streptophyta; Er
yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPE
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Pred. No. 1.9e
L3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
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                                                                                                                                             Embryophyta; Tracheophyta;
; Poales; Poaceae; Pooidea
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L.9e-11;
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PRECURSOR.
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(AX2*).
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                                                                                                                                               Pooideae;
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Best Local S
Matches 87
Query Match
Best Local S
Matches 94
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Q20189;
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SIGNAL
                                                           VARSPLIC
SEQUENCE
                                                                                                                 EMBL; Z69791; CAA93662.1; -.
EMBL; Z69791; CAA93660.1; -.
EMBL; Z69791; CAA93661.2; -.
EMBL; Z69791; CAA93661.2; -.
Hypothetical protein; Alternative splicing.
VARSPLIC 1 15
MNILLNYCNILISIK
                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel 01, Created)
01-AUG-1998 (TrEMBLrel 07, Last sequence up
01-JUN-2001 (TrEMBLrel 17, Last annotation
HYPOTHETICAL 99.1 KDA PROTEIN F39D8.1C.
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Theor. Appl. Genet. 83:373-378(1
EMBL, X61009; CAA43331.1; -.
Mendel; 14738; Triae;2380;14738.
InterPro; IPR001419; Glutenin.
                                                                                                                                                                                                                Submitted (FEB-1996)
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                                                                                               VARSPLIC
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
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nes 87; Conserv
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                                                                                                                                                                              F39D8.1B AND ISOFORM ALTERNATIVE SPLICING.
                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGQQLRQGQQGQQSGQGQPRYYPTSSQQPGQLQQLAQGQQGQQPERGQQG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQGQGQGQG-QGQGQGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQ-QQSNEYGRPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YG--GNQNSNGQHESFNFSGNFSQQNNNGNQNR
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94;
            Similarity
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924
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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            16.0%;
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JCTS: THREE FORMS; ISOFORM F39D8.1A,
FORM F39D8.1C (SHOWN HERE); MAY BE P
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                                                        F39D8.1B).

Q -> QYVLNVPTNYLQVPSTSNR (:
F39D8.1A).
F39D8.1A).
A -> AVKA (IN F39D8.1A).
A -> AVKA (IN F39D8.1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPE
 27;
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Pred. No. 2.9e
13; Mismatches
            Score
Pred.
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HIGH MOLECULAR WEIGHT GLUTENIN SUBUNIT
1AX1.
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 Mismatches
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            216; DB 5;
No. 3.1e-11;
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 109;
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                      Length 924;
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 124;
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RESULT
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                                                           Query Match
Best Local Similarity
                                                Matches
                                                                                                         SEQUENCE FROM N.A.
Anderson O.D., Greene F.C.;
Anderson O.D., Greene F.C.;
Theor. Appl. Genet. 0:0-0(0).
EMBL; x13927; CAA32115.1; -
EMBL; M22209; AAA34291.1; -
Mendel; 14744; Triae; 2380; 14744.
InterPro; IPRO01419; Glutenin.
PRINTS; PRO0210; GLUTENIN.
SEQUENCE 789 AA; 84638 MW; CFU
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Q42451;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               υναιγοια; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
Triticeae; Triticum.
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Search completed: February 1, 2002, 15:07:12 Job time: 317 sec

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Q02630;
Q01-UUL-1993 (Rel. 26, Created)
Q1-UUL-1995 (Rel. 33, Last sequence update)
Q1-FEB-1996 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1996 (Rel. 36, Last sequence update)
Q1-NOV-1997 (Rel. 36, Last sequence update)
Q1-NOV-1
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MEDILINE-93054906; PubMed-1385442;

Wente S.R., Rout M.P., Blobel G.;

"A new family of yeast nuclear po
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear pore protein NSP1."
EMBO J. 11:5051-5061(1992).
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Wimmer C., Doye V., Grandi P., Ne
"A new subclass of nucleoporins t
nuclear pore protein NSP1.";
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                                       L; 215036; CAA78754.1; X68108; CAA48228.1; X68108; CAA88413.1; X68502; CAA88413.1; X28537; S28537; S28537; S28537; S28925; S28925; S28925; S444402; A44402;
                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss institute or institute. There are no rest European Bioinformatics Institutes as long as its content by non-profit institutions as long as its content by non-profit institute or institutions as long as its content by non-profit institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: INTERACTS WITH KAP95.
SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.
DOMAIN: CONTAINS G-L-F-G REPEATS.
SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                        cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two dissimilar domains linked by an asparagine/glutamine-rich sequence."; Mol. Microbiol. 6:1013-1023(1992).

-i- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES AND DOMAIN 2 MORE XYLOSE.

-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.
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01-DEC-1992
15-JUL-1999
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                                 PATHWAY: XYLAN DEGRADATION.
SIMILARITY: IN THE N-TERMINAL SECTION;
G (FAMILY 11 OF GLYCOSYL HYDROLASES).
SIMILARITY: IN THE C-TERMINAL SECTION;
F (FAMILY 10 OF GLYCOSYL HYDROLASES).
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    SWISS-PROT entry
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rmicutes; Bacillus/Clostridium
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(Rel. 38, Last annotation update)
ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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37 x 6 AA APPROXIMATE R
G-L-F-G.
G -> A (IN REF. 1).
S -> G (IN REF. 1).
S -> Y (IN REF. 1).
S -> Y (IN REF. 1).
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      a collaboration
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Best Local
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01-MAR-1989 (Rel. 10, Crebted)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 P
GLU-1D-1D OR GLU-D1-1B.
Triticum aestivum (Wheat).
                                                                                                                                    GLT5_WHI
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InterPro; IPR001137; Glyco_hydro_11.
Pfam; PF00331; Glyco_hydro_10; 1.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00134; GLHYDRLASE10.
PRINTS; PR00911; GLHYDRLASE11.
PROSTIE; PS00591; GLYCOSYL_HYDROL_F10;
PROSTIE; PS00591; GLYCOSYL_HYDROL_F10;
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the Euro
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PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Xylan degradation; Hydrolase; Glycosidase; Multifunctional enzyme;
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Pred. No. 3.5e
44; Mismatches
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PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
1; 1033567D4B526EBD CRC64;
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XYLANASE DOMAIN 2.
NUCLEOPHILE (BY SIMILARITY)
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MEDLINE=89098419; PubMed=2563152;
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Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
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InterPro; IPR001419; Glutenin.
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SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
MISCELLANBOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF GROUP 1 CHROMOSOMES OF WHEAT.

MISCELLANBOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGO AND
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GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLT4_WHEAT P08489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. YAMHILL;
MEDLINE=86093674; PubMed=3001648;
Sugiyama T., Rafalski A., Peterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _WHEAT
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01-AUG-1988 (Rel. 08,
15-JUL-1999 (Rel. 38,
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MISCELLANGOUS: THE MATURE PROTEIN IS CHARACTERIZED I UNBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS:
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Pred. No. 3.
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71D715B7BDF0722D
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                                          "An RNA-binding protein gene, TLS/FUS, is fused to ERG in hum myeloid leukemia with t(16;21) chromosomal translocation."; Cancer Res. 54:2865-2868(1994).
                                                                                                                                                                              SEQUENCE OF 265-276; 317-331 AND 335-357, AND IDENTIFICAT MEDLINE-99369251; PubMed-10442642; Bertrand P., Akhmedov A.T., Delacote F., Durrbach A., Lop "Human POMp75 is identified as the pro-oncogene TLF/FUS: POMp75 and POMp100 DNA homologous pairing activities are to cell prolifieration.";
                                                                                                                                                                                                                                                                                                                                                                                              Morohoshi F., Ootsuka Y., Arai K., Ichikawa H., Munakata N., Ohki M.; "Genomic structure of the human RBP56/hTAFII68 Gene 221:191-198(1998).
                                                                                                                      CHROMOSOMAL TRANSLOCATION. MEDLINE=94243799; PubMed=8187069;
                                                                                                                                                                Oncogene
                                                                                                                                                                                                                                                                                        Baechtold H., Kuroda M., Sok J., Ron D., Lopez B.S "Human 75-kba DNA-pairing protein is identical to TLSZFUS and is able to promote D-loop formation."; J. Biol. Chem. 274:34337-34342(1999).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=20036580; PubMed=10567410; Baechtold H., Kuroda M., Sok J., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS). MEDLINE-99013873; PubMed-9795213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Fusion of the dominant negative transcription regulator CHOP with a novel gene FUS by translocation t(12;16) in malignant liposarcoma."; Nat. Genet. 4:175-180(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 235-244; 307-312; 335-345 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT ISOFORM). MEDLINE-93350637; PubMed-7503811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Fusion of CHOP to a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPOSARCOMA
FUS OR TLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P35637;
01-JUN-1994
                                                                                                                                                                                                                                                                           [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabbitts T.H., Forster A., Larson R., Nathan P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 363:640-644(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE=93288139; PubMed=8510758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475
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                                                                                                                                                                  18:4515-4521(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
PROTEIN FUS (ONCOGENE FUS) (ONCOGENE TLS) (TRANSLOCATED
PROTEIN) (POMP75). (75 KDA DNA-PAIRING PROTEIN).
ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P., Mandahl N., Ron D.;
to a novel RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GRPQY - - - GGNONSNGQHE - - - SFNFSGNFSQQNNNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ichikawa H.,
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                                                                                                                                                                                                are associated
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                                                                                                                                                                                                                              B.S.;
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CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
ZN_FING
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Pfam; PF00641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S62140; AAB27102.1; --
EMBL; S62138; AAB27103.1; ALT_SEO.
EMBL; X71427; CAA50558.1; ALT_SEO.
EMBL; X71428; CAA50559.1; ALT_SEO.
EMBL; AF071213; AAC35285.1; --
EMBL; AF071213; AAC35284.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; P09651; 1HA1.
MIM; 137070; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1;
Proto-oncogene; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-RanBP
      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: A FORM OF MALIGNANT MYXOID LIPOSARCOMA IS CHARACTERIZED BY A CHOMOSOMAL TRANSLOCATION T(12;16)(Q13;P11) THAT INVOLVES EVEN TO THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML) BY A CHROMOSOMAL TRANSLOCATION T(16;21)(P11;Q22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrictions of the contract of th
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                                                                                                                                                                                                                                                                                                                                                                                         MNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGY 92
      QSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQN
                                                                  SYGQQSSYPGYGQQPAPSS---
                                                                                                                                                                                                 GQQSY----SGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSTGGYGSSQSSQS
                                                                                                                                                                                                                                                          NNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQ 152
                                                                                                                               GQNYQHQQQGQQQQGHSSSFSALASMASSYLGNNSNSSSYGGQQQANEYGRPQHNGQQ
                                                                                                                                                                                                                                                                                                                          MASNDYTQQAT-----QSYGAYPTQPG------QGYSQ-----QSSQPY
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526 AA;
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ene; RNA-binding; DNA-binding; Nuclear protein; Repeat;
splicing; Chromosomal translocation; Zinc-finger; Zinc
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUS/TLS-CHOP ONCOGENE.
TG -> S (IN SHORT ISOFORM).
T -> N (IN REF. 4).
88C8E263B7905549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANBP-TYPE.
BREAKPOINT FOR TRANSLOCATION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARG/GLY-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEINS
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SPLICING.
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L outstation -
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N100_YEAST
Q02629;
Q1-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in entities requires a license arresmond. Usage by sand an entities requires a license arresmond.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNOWN PROTEINS,";
Yeast 10:569-S74(194).
-i- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION
THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93054906; PubMed-1385442; Wente S.R., Rout M.P., Blobel G.; "A new family of yeast nuclear pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
NUCLEOPORIN NUP100/NSD100 (NUCLEAR PORE PRO
                                                                                                                                                                                                                                                                    SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wente S.R., Rout M.P., Blobel G.
"A new family of yeast nuclear p
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUP100 OR NSP100 OR YKL068W OR YKL336
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94378724; PubMed=8091863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of a 20.7 kb region of yeast chromosome XI includes the
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                                                                                                                                                                                                                                   Nuclear protein; Transport; Repeat.
DOMAIN 33 571 29 X 6
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                            -NOSSGGSSFGALASMASSFMHS----NNNQNSNNSQQGYNQSYQNG-----NQNSQGY 92
                                                                                         GQGQGQGQGQGQGQGGSFTALASLASSFMNSNNNNQQ----GQ--
                                                                                                                                                                                                                                                                    S0001551; NUP100.
                                                             GNSNNNNNSTSNNAQSGFGGFTSAAGSNSNSLFGNNNTQNNGAFGQSMGATQNSPFGSLN
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                                                                                                                        Score 215.5; DB Pred. No. 5.1e-077; Mismatches 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                   Hypothetical protein SEQUENCE 401 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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30-MAY-2000
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                                                                                                                                                                                              TELLESNVYANEMNMLMGSSSAPLQQYRAYAGCSSSGCVPATIVPKSSGEWPNADMIAGL
         SSYGGQQQANEYGRPQHNGQQQSNE--YGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGN
                                                             NNQQQYQQQQ-----NYQHQQQGQQQQ-QGHSSSFS--ALASMASSYLGNNSNSN----
                                                                                                                                           QTEQRSQNQNQNSNNPQQDDPRTSQSTGQINGNVPGSSSSNQQPVIYIARAGSDKYKNSE
                                                                                                                                                                    ASSEMHSNUNQUSUNSQQGYNQSYQ----NGNQNSQGYNNQQ-
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                                    NNFQQNQNLGASSGFFNNQNQQNSQQNQVNGPTSGFSNQQTSNQNSGFFNNQNQQNGQNF
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                                                                                                                                                                                                                                                                                                                                                        Z32679; CAA83596.1;
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                 ----Y0GGN---GGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQ
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cinae; Caenorhabditis.
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Pred. No. 4.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mycetozoa; NCBI_TaxID=44689;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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SYGGQQQANEYGRPQHNGQQQSNEYGR----PQYGGNQNSNGQHESFNFSGNFSQQNNNG
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                                                                                                                                                                                                                                                                                                                    SSIMSSNVFPSHDGQ-----YPDMPNMVDQYQIHPNQNPH-----YNYQYQLMFM 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation;
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292
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79268
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29.6%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 207; DB 1;
Pred. No. 1.3e-06;
7; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 10
FUS_MOUSE
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                                                                                        Query Match
Best Local :
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Regulation of pigpen expression in mouse embryos.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND
-I- FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNA. MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY (BY
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P56959;
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alappat S.R.,
Burdsal C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUS_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF224264; AAF70602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR002952; Eggshell.
InterPro: IPR000504; RRM.
InterPro: IPR001876; Znf-RanBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM). SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:1353633; Fus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON
                                                                 l Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                          PS50102; RRM; 1.
PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang M., Zhao X.,
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                                                                                                                                                               167
265
364
518
440
52673
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40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                        15.0%;
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                                                                                                                                                                                 X.
                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Repeat; Zinc-finger; Zinc;
                                                                   25;
                                                                                        Score
Pred.
                                                                                                                                                                          RNA-BINDING (RRM).
ARG/GLY-RICH.
C4-TYPE (POTENTIAL).
; E06F231BFEED78D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Bioinformatics
                                                                                                                                                                                                                                                                      GLN/GLY/SER/TYR-RICH GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alliegro M.A.,
                                                                      3 202; L.
No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
                                                                                                           DB 1;
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                                                                                                           Length
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                                                                 Indels
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                                                                                                              518;
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FUS_BOV
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01-NOV-1997
20-AUG-2001
RNA-BINDING
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Q28009;
                                                                                                                                                                                                    This
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Bovidae; Bovinae;
                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                    <del>'</del>-
                                                                                                                                                                                                                                                                                                                                                                                                                              <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                  U26024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN
                     AAC13543.1;
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use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                        regulatory protein, pigpen: new function for an EWS family member.";
EXP. Cell Res. 255:270-277(2000).
-: FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNA. MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A nuclear protein regulated during quiescent phenotype in cultured endo Dev. Biol. 174:288-297(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alliegro M.C.; "A C-terminal carbohydrate-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96175600; PubMed=8631501;
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                                                                                                                                                                                               DOMAIN: THE C-TERMINAL DOMAIN BINDS CARBOHYDRATES. SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM). SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR, EXHIBITS DIFFUSE S'
SUBCELLULAR LOCATION: NUCLEOLI), TOGETHER WITH A
THROUGHOUT (EXCLUDING NUCLEOLI), TOGETHER WITH A
                                                                                                                                                                                                                                                                          INTENSELY STAINED FOCAL POINTS, ALONG THE NUCLEAR ENVELOPE.
                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: COMPONENT OF
                                                                                                                      SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBL
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email to license@isb-sib.ch).
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(Rel. 35, Last sequence up)
(Rel. 40, Last annotation
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Best Local :
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P18899;
01-NOV-1990
01-FEB-1996
30-MAY-2000
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DOMAIN
ZN_FING
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"Structure of the DNA damage-inducible goits role in mutagenesis in Saccharomyces Mol. Cell. Biol. 10:3174-3184(1990).
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                                     Tonouchi A., Fujita A., Kuhara S. "Molecular cloning of the gene en SFL1 gene-disrupted flocculating J. Blochem. 115:683-688(1994).
                                                                                                                                                                                   [2]
[2]
                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Pfam; PF00641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
  SEQUENCE
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MEDLINE=90258909; PubMed=2111448;
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                         SEQUENCE FROM N.A.
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InterPro; IPR001876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        N-1990 (Rel. 16, Created)
N-1996 (Rel. 33, Last sequence update)
N-2000 (Rel. 39, Last annotation update)
STRESS PROTEIN (DNA DAMAGE-RESPONSIVE PROTEIN 48) (DDRP 48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESGNESQQNNNGNQNR
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Similarity 28.8%;
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ARG/GLY-RICH.
C4-TYPE (POTENTIAL).
W; 3652329C044F1386 C
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Pred. No. 3.3e-06;
0; Mismatches 110;
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GLY-RICH.
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PIR; A45429; A45429.
SGD; S0004784; DDR48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and characterization of Saccharomyces cerevisiae DNA damage-responsive protein 48 (DDRP 48).";
J. Biol. Chem. 268:4752-4758(1993).
-1- FUNCTION: DISPENSABLE FOR ACQUISITION OF THERMOTOLERANCE AND DOES NOT PLAY A SIGNIFICANT ROLE IN RECOVERY OR PROTECTION OF CELLS FROM ACUTE HEAT SHOCK. MAY BE IMPLICATED IN ONE OR POSSIBLY MORE PATHWAYS OF MUTAGENESIS IN YEAST. HYDROLYZES ATP AND GTP YIELDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-30. MEDLINE-93186777; PubMed-8444852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unurcher C.M., Barrell B.G., Submitted (JUN-1995) to the F
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Churcher C.M., Barrel
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S73336; AAB31954.1;
Z49808; CAA89906.1;
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RET 0 0 8 AA:

73 413 8 AA:

(CT 37 37 E -> (
CCT 37 45102 MW; 0A2)
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TO S.POMBE SPAC23H3.15C.
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-> Q (IN REF. 1).
0A26FF5885D6BA2E CRC6
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No. 4.
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DOMAIN
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"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters asparagine, glutamine, or threonine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC-RICH MRNA CLONE AAC11 PROTEIN (FRAGMENT).
DICTYOSTE11um discoideum (Slime mold).
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DictyDb; DD05006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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348
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                                                                                                                                                                                       NINNNNNNNNNNNNNNNNSNLGINSSPTQSSANSADKRSRGRPRKNPPSEPKDTSGPKRKR 185
                                                                                                                                                                                                                                   GGNNGNNSGNNNGQPQMHGTNLNGLSLAIQNQSSLPQPINNNNNNNNNNS---
                                                                                                                                                                                                                                                           GQGQGQGQGQGQGQGSFTALASLASSFMNS-----NNNNQQGQNQSSGGSSFGALA 56
NONTNUNMGNNSNNNNNPNNNH
                      GQHESFNFSGNFSQQNNNGNQNRY
                                                                   SSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQQQSNEYGRPQYGGNQNSN 229
                                                                                                                 GGA--FSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGH
                                                                                                                                        GRPPKMDEEGNPQPKPVPQPGSNKKRGRPKKPKDENESDYNNTSFSDSNTDGTPKKRGRP
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                                                                                           -----YQNGN-----------QNSQGYNNQQYQGGN-GGYQQQQGQS 111
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an email to license@isb-sib.ch).
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ASN-RICH.
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RESULT 14
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P084488;
01-AUG-1988 (Rel. (
01-AUG-1988 (Rel. (
15-JUL-1999 (Rel. :
                                                                                                                                                                                                                                                                                          DOMAIN
SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea

Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. CHINESE MEDLINE=86041882;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X03041; CAA26847.1; -.
PIR; A24266; A24266.
HSSP; P01088; 1BFA.
InterPro; IPR001768; Cereal_tryp_amyl_inh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BER RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-i- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-i- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMW-glutenin subunit.";
Nucleic Acids Res. 13:6833-6846(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Nucleotide sequence of a gene from chromosome
421
                           153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROUP 1 CHROMOSOMES OF WHEAT.
MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED I
NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQQPGQGQQGYYPTS.
                                                                                                                                                                                                                                                                                                                                                             storage protein;
                                                                                                                                                                                            GQGQGQGQGQGQGQ-------GQGSFTALASLASSFMNSNNNNQQGQ-----
GQGQQGYYPTSLQQPGQGQQQQGQGQGYYPTSLQQPGQGQQGHYPASL-
                          GQNYQH-----QQQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRP
                                                     GQQGHYPASLQQPGQQGHYPTSLQQLGQGQQIGQPGQKQQPGQGQQTGQGQQPEQE-QQP
                                                                               GGNGGYQ---QQQGQSGGAFSSLASMAQ-SYLG--GGQTQSNQQQYNQQGQNNQQQYQQQ 152
                                                                                                            QQQPGQGQQG-----HYPASQQQPGQGQGHYPASQQEPGQGQQGQIPASQQQPGQ
                                                                                                                                   NOSSGGSSEGALASMASSEMHSNNNQNSNNSQQG-YNQSYQNGNQNSQGY----NNQQYQ
                                                                                                                                                                  GQGQQPGQWQQSGQGQQGHYPTSLQQPGQGQ-----QGHYLASQQQPAQGQQGHYPAS 310
                                                                                                                                                                                                                                                                                                                                                                                         PF00234; tryp_alpha_amyl;
                                                                                                                                                                                                                        86;
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PubMed=3840588;
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70868 MW;
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20-AUG-2001
EMBL;
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                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
MEDLINE-97124846; PubMed-8954779;
MOROCHOSHI F., Arak H., Takahashi E.-I., Tanigami A.,
"Cloning and mapping of a human RBP56 gene encoding &
"Cloning and mapping of a human RBP56 gene encoding &
binding protein similar to FUS/TLS and EWS proteins."
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 221:191-198(1998)
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TAF2N OR RBP56.
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20-AUG-2001 (Rel. 40, Last annotation u
TATA-BINDING PROTEIN ASSOCIATED FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Munakata M., Ohki M.; "Genomic structure of the human RBP56/hTAFII68 and FUS/TLS genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS). MEDLINE-99013873; PubMed-9795213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase II.";
EMBO J. 15:5022-5031(1996).
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SUBUNIT: BELONGS TO THE RNA POLYMERASE II (POL II) TRAISUBUNIT: BELONGS TO THE RNA POLYMERASE II (POL II) TRAISULTIPROTEIN COMPLEX, TOGETHER WITH THE TATA-BINDING PI AND OTHER TBP-ASSOCIATED FACTORS (TAF(II)S).

SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

AUTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOW AND A SUBCRIFICATIVE SPLIC TISSUE SPECIFICITY: UBIQUITOUS. OBSERVED IN ALL FETAL
                                                                                                                                                                           DISEASE: A FORM OF EXTRASKELETAL MYXOID CHONDROSARCOMAS (EMC) CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(9;17)(Q22;Q11) INVOLVES TAFZN AND NR4A3: SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM). SIMILARITY: CONTAINS 1 RANBP-TYPE ZINC FINDER. SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: "RNA AND SSDNA-BINDING PROTEIN THAT MAY PLAY SPECIFIC ROLES DURING TRANSCRIPTION INITIATION AT DISTINCT PROMOTERS. CAN ENTER THE PREINITIATION COMPLEX TOGETHER WITH THE RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GQRQQPGQGQHPEQGQQPGQGQQGYYPTS---PQQPGQGQQ
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X98893; CAA67398.1;
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ISNPMSTEDRN 0;	IQIRVMGASNRLMSMVDRN', 'RMVNSNPMSTEDRN N:AAA34615.1; PID:g171536 	VHSQLWLPWQVPTWAITP ; NID:g171534; PID ; NID:g171534; PID ; Score 1347; D %; Pred. No. 8.5e %; Pred. No. 8.5e
ence for a	g yeast conjugation: evide	A;ACCESSION: 51/4/1 A;Status: translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-186 <ram> A;Residues: 1-186 <ram> A;Cross-reterences: EMBL:S58084 A;Cross-reterences: EMBL:S58084 A;Cross-reterences: EMBL:3286, 1987 MOL. Cell. Biol. 7, 2316-2328, 1987 A;Title: Two genes required for cell fusion during A;Reference number: A93093; MUID:87286864 A;Accession: C27061 A;Molecule type: DNA</ram></ram>
0; PID:g533 C.P.	:CAA42357.1; PID:e26443 inhans, U.; Hollenberg, ent from ClG on chromos	; NID:g1907116; PII hen, K.; Xu, G.; K of a 11,953 bp frac D:91377317
<u>.</u>	es cerevisiae) 2 #text_change 29-Oct-1999 K.; Ramezani Rad, M.; Xu,	RESULT 1  \$19355  N;Alternate names: hypothetical protein YCL028w - yeast (Saccharomyce N;Alternate names: hypothetical protein YCL181 C;Species: Saccharomyces cerevisiae C;Date: 31.Mar.1992 #sequence_revision 31.Mar.1992 (C;Accession: \$19355; \$17471; \$C27061 R;Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, submitted to the Protein Sequence Database, March A;Reference number: \$19350
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hing part to the confirmation of the confirmat	heat shock protein RNA/SsDNA-binding ANA/SsDNA-binding hypothetical prote glutenin high mole hypothetical prote hypothetical prote repetin - mouse gene mastermind pr hypothetical protein bypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein finger protein AZF glutenin high mole lustrin A - Califo notch protein - fr CLOCK protein - fr	30 195.5 14.5 430 1 HHBYD8 31 195.5 14.5 589 2 S71954 32 194 14.4 448 2 S05355 33 194 14.4 660 2 A24266 34 192 14.3 465 2 F75524 35 191.5 14.2 697 2 T16306 36 191 14.2 1130 2 T30251 37 190.5 14.1 1655 2 T13998 38 189 14.0 282 2 T20402 39 189 514.0 1655 2 T20402 40 188.5 14.0 549 2 T20720 41 188.5 14.0 549 2 T20720 41 189.14.0 914 2 S46593 42 187.5 13.9 648 2 T204832 43 187.5 13.9 1428 2 T04832 44 187.5 13.9 1428 2 T04832 45 187.5 13.9 1428 2 T04832 46 187.5 13.9 1428 2 T04832 47 187.5 13.9 1428 2 T04832 48 187.5 13.9 1428 2 T04832 49 188.5 13.9 1428 2 T04832 40 188.5 13.9 1428 2 T04832 41 189.5 13.9 1428 2 T04832

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hypothetical protein F21C10.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_C;Accession: T29339
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F21C10.
A;Reference number: Z20610
A;Accession: T29339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-382 <DUZ>
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A;Residues: 1-3498 <WIL>
A;Cross-references: EMBL:Z49888; PIDN:CAA90064.1;
A;Experimental source: clone F47A4
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PIDN:AAA97972.1; GSPDB:GN00023;
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0; Mismatches 117; Indels
                                                                                               cosmid F21C10
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A;Map position: 5
A;Introns: 20/1; 219/3;
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A; Residues: 1-409 <WIL>
A; Cross-references: EMB
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A;Gene: CESP:F13E9.4
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                  NVSSSAAQDYYNIVNNKSLTTNQINEQASNWASANSVQAQYIQYETNRSAIHTQATQNVS
                                                GGQTQSNQQQY----
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                                                                                NGNNN----QGSSSGYQNNQGRHQGQGGGHSSSSNSVMSNNGYSSNSGYGNNNGPTPSFLN
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ze: clone F13E9
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27.98;
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28.7%;
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                                                                                                                                                                                                                                                                                            Score 232; DB 2;
Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 237; DB 2
Pred. No. 3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
                                               NOOGONNOOOYOOOGONYOHOOOGO----OOOOGHS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 1996
                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                            Length 409
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15-Oct-1999

Indels

90;

Gaps

15

AQSYLG 127

180

237

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15 QGQGQGSFTALASLASSEMNSNNNNQQGQNQSSGGSSFGALASMASSEMHSNNNONSNNS 74
                            ANEYGRPQHNG-QQQSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNN 247
                                                                                                   TLPSVNNSEPNIPTMPTAPCLCNAQNCGNTTNTNAIGNTPQRDAYGNQMGSNSQFQQ
                                                                                                                                                                                                                                                               QSYLGGGQTQSNQQQYNQQGQNNQ--QQYQQQGQNYQHQ-QQGQQQQQQGH-----SSSFS 174
                                                                                                                                                      ALASMASSY------QQ 199
                                                                                                                                                                                                               DYSFNNGNCQYKDGQVIENGQTRQATQQELQQIQQYRNSVDQYMNQVNGYVGQWINSVFQ
                                                                                                                                                                                                                                                                                                                        QQGQQNNYGTQAQYDAGQNQMGQSGQVQGYSNNGYSNQNSQMSQSQASSG---SSSVSLM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                    QNQQYGS-----TAQYNQNQMQNQQNSNQYSTTSNM------NNQQNSNQY 112
ANQNGQYQNTQYQQQNGQNGQNQF---QQSNGQNQNSQYQQTSNQQMNN
                                                                                                                                                                                                                                                                                                                                                                              QQGYNQSY-----QNGNQNS------QGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone F21C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
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A; Map position: 13R
C; Keywords: nucleus
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A;Residues: 1-25,'A',27-535,'G',537-719,'P',721-1017,'Y',1019-1022,'Y',1024-1113 <WEN>
A;Residues: 1-25,'A',27-535,'G',537-719,'P',721-1017,'Y',1019-1022,'Y',1024-1113 <WEN>
A;Cross-references: EMBL:215036; NID:94075; PIDN:CAA78754.1; PID:94076
A;Note: sequence extracted from NCBI backbone (NCBIP:117132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1113 <WIN>
A;Residues: 1-1113 <WIN>
A;Cross-references: EMBL:X68108; NID:g4052; PIDN:CAA48228.1; PID:g4053
A;Cell Biol. 119, 705-723, 1992
A;Title: A new family of yeast nuclear pore complex proteins.
A;Reference number: A44402; MUID:93054906
A;Accession: A44402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 21-Jul-2000
C;Accession: S28925; A44402; S52896; S28537
R;Wimmer, C.; Doye, V.; Grandi, P.; Nehrbass, U.; Hurt, E.C.
EMBO J. 11, 5051-5061, 1992
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A; Residues: 1-1113 <ODE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Odell, C.; Bowman, S. submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: A new subclass of nucleoporins that A;Reference number: S28026; MUID:93099880 A;Accession: S28925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear pore complex protein NSP116 - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SGD:NUP116; NSP116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S52885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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  224 GNQNSNGQHESFNFSGNFSQQNNNGNQ
                                                                                                                                        383
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                                                          SKPAGGLFGQQQGASTFASGNAQNNSIFG---
                                                                                                                                    LFGQTNQQQSGGGLFGQQQNSNAGGLFGQNNQSQNQSGLFGQQNSSNAFGQPQQQGGLFG
                                                                                                                                                                        GQTQSNQQQ----YNQQ-----GQNNQQQYQQQ--GQNYQHQQQGQQQQQGHSSS 172
                                                                                                                                                                                                              QGSGGIFGQSNANANGGAFGQQQGTGALFGAKPASGGLFGQSAGSKAFGMNTNPTGTTGG
                                                                                                                                                                                                                                                        GGNGG----
                                                                                                                                                                                                                                                                                        NTTNNPTNGTNNTGLFGQQNSNTNGGLFGQQQNSFGANNVSNGGAFGQVNRGAFPQQQTQ 322
                                                                                                                                                                                                                                                                                                                            NNNQNSNNSQQ-----GYNQSYQNG----NQNSQGYNN---------QQYQ 98
                                                                                                                                                                                                                                                                                                                                                                GTGTGSGGGFGSGATNSTGL-----FGSSTN-----LSGNSAFGANKPATSGGLFG 262
                                                                                                                                                                                                                                                                                                                                                                                                        GOGQGQGQGQGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMASSFMHS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYGGNQNSNGQHESFNFSGNFSQQNNNGNQNRY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIINNLATVQASIEGIQSNTSSSENDRQSAFQALQQAHPMEYSVLTSLQNQHEQTQYAR-
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                                                                                                  FSALASM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MGSNGNSNSNYGNSNFNSNYGNNGYNHNGNNY 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S52896
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD:S0004650; MIPS:YMR047c
                                                                                              ASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQQQSNEYGRPQYG---
                                                                                                                                                                                                                                                    ---YQQQQG------QSGGAFSSLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 224.5; DB 2;
Pred. No. 5.8e-08;
8; Mismatches 97;
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                                                            -GGLF 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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S18733
                                                      C; Superfamily: glutenin
                                                                                              A; Molecule type: DNA
A; Residues: 1-705 <HAL>
                                                                                                                                                    A; Reference number: S18733
A; Accession: S18733
                                                                                                                                                                                                Theor. Appl. Genet. ....
                                                                                                                                                                                                                              R; Halford, N.G.; Forde, Theor. Appl. Genet. 75,
                                                                                                                                                                                                                                                                  C; Accession: S18733
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A; Accession: T40875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-658 < WOO1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T41309; T40875
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                                                                                                                                A; Status: preliminary
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Query Match
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                                                                                                                                                                                                            and
16.5%;
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A;Cross references: EMBL:AL022245; NID:94584240; PIDE A;Experimental source: strain 972h-; cosmid c320 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, submitted to the EMBL Data Library, September 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1998 A;Reference number: Z21986 A;Accession: T41309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 468-658 <WOO2>
A;Cross-references: EMBL:AL031764; NID:g3668147;
A;Experimental source: strain 972h-; cosmid c123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical threonine/asparagine-rich protein C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-199
A;Cross-references: EMBL:X61026; NID:g22089; PIDN:CAA43361.1; PID:g22090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 QGSSGGLSAAAVSGLIGSFMGSSSNNSNSSNNNSNTSNNNSNTSNNESMVSKLSSLSGMA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V.; Rajandream, M.A.; Barrell, B.G.; Wedler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGLASSFLNSSSGNSNKQNYN--NNNNQNYGNNNNQNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASSYLGNNSNSNSSYGGQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHSSSFSALAS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSFLGSSGNNNNNNNSGS-----NYNNNNSGNNNOOHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSFM-HSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                       - NNNNNSSQGGNSQ
                                                                                                                                                                                       J.; Anderson, O.D.;
117-126, 1987
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                                                                                                                                                              deduced
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Pred. No. 5.2e-08;
                                                                                                                                                            amino acid sequences of an HMW glutenin subunit
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                                                                                                                                                                                                          Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c1235
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                                                                                                                                                                                                          F.C.; Shewry,
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Score 222;

DВ

Length 705;

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R:Kuspa, A.; Lu, S.; Souza, G.M.
submitted to the EMBL Data Library, January 1998
A:Description: YakA, a protein kinase required fc
A:Reference number: Z18146
A:Recession: T1457
A:Status: preliminary; translated from GB/EMBL/DI
A:Molecule type: mRNA
A:Residues: 1-1457 <KUSS
RESULT 9
B30843
glutenin high molecular weight chain
C;Species: Triticum aestivum (common
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C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific
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C;Genetics:
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Best Local S
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                                                                                               KQQQKNLHHQQQQQQQRFMQVGSP
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Pred. No. 1.9e-07;
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4; Mismatches 141;
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 Ax2 precursor wheat)
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A; Gene: xynA
A; Start codon:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N:Contains: endo-1,4-beta-xylanase (EC 3.2.1.8) precursor, bifunctional - C;Species: Ruminococcus flavefaciens (EC 3.2.1.8) c;Jate: 22-Nov-1993 #sequence_revision 22-Nov-1996 #text_chang C;Accession: S20907; S18043 R.Zhana .Tv . Elic. ...
                                                                                   A; Pathway: xylan degradation

G; Superfamily: Ruminococcus bifunctional endo-1,4-beta-xylanase; endo-1,4-beta-xyla

G; Superfamily: Ruminococcus bifunctional endo-1, 4-beta-xylanase; multifunctional enzyme;

C; Keywords: extracellular protein; glycosidase; hydrolase; multifunctional enzyme;

F; 1-27/Domain: signal sequence #status predicted <SIG>
F; 28-954/Product: bifunctional endo-1, 4-beta-xylanase #status predicted <CDA>

F; 28-248/Domain: catalytic domain A #status predicted <CDA>

F; 20-236/Domain: endo-1, 4-beta-xylanase homology <XYL>

F; 40-236/Domain: endo-1, 4-beta-xylanase homology <XYL>
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C;Accession: B30843
R;Anderson, O.D.; Gre
submitted to GenBank,
                    F;249-622/Domain: linker region B *status predicted <LRB>F;623-954/Domain: catalytic domain C *status predicted <CDC>F;655-953/Domain: Streptomyces endo-1,4-beta-xylanase A homology
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-954 <ZHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Zhang, J.X.; Flint, H.J.
Mol. Microbiol. 6, 1013-1023,
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C;Keywords: seed; storage
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A; Residues: 1-815 < AND>
                                                                                                                                                                                                                                           A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
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Best Local Similarity
Matches 87; Conserv
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ce: strain 17
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  Glu #status
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31.9%;
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Pred. No. 1.
predicted
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A;Title: Nucleotide sequences of the two high-molecular-weight glutenin genes A;Reference number: S02262; MUID:89098419
A;Accession: S02262
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C;Superfamily: glutenin
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A; Residues: 1-848 <AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutenin high molecular weight chain Dx5 - wheat C;Speckes: Triticum aestivum (common wheat) C;Deckes: Freb-1990 #sequence_revision 28-Feb-1990 #text_change 03-Feb-1994 C;Accession: S02262
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               GQQPGQGQPGYYPTSPQQSGQGQPGYYLTSPQQSGQGQQPGQLQQ-SAQGQKGQQPGQCQ
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                                                                                                                                                                                                                             FSSLASMAQSYLG-----GGQTQSNQQQYNQQGQ--NNQQQYQQQGQNYQHQQQGQ 163
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                                                       -----PQHNGQQQSNEY-GRPQYGGNQNSNGQHESFNFSGNFSQQNNNGN 249
                                                                                                                                                                                                                                                                                                               SEMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGY-----QQQQQGQSGGA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%; Score 217.5; DB 2; llarity 29.9%; Pred. No. 1.3e-07; Conservative 13; Mismatches 133;
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A;Note: the authors translated the codon CTA for residue 11 as Val, CAT for residue 4 C;Comment: The main wheat storage proteins are divided into two groups. The glutenins
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-838 <SUG>
A; Cross-references: GB:X03346; NID:g21784; PIDN:CAA27052.1; PID:g736319
A; Experimental source: cv. yamhill
C; Comment: Glutenins, like gliadins, are high in glutamine and proline to c; Superfamily: glutenin
C; Keywords: seed; storage protein
C; Keywords: seed; storage protein
C; Keywords: seed; storage protein
                                                                                                                                                                              R:Sugiyama, T.; Rafalski, A.; Peterson, D.; Nucleic Acids Res. 13, 8729-8737, 1985 A;Title: A wheat HMW glutenin subunit gene 1 A;Reference number: A24107; MUID:86093674 A;Accession: A24107
                                                                                                                                                                                                                                                                   glutenin, high molecular weight chain precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999 C;Accession: A24107 R;Sugiyama, T.; Rafalski, A.; Peterson, D.; Soll, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: Ax2*
C;Superfamily: glutenin
F;1-21/Domain: signal sequence #status predicted <
F;22-815/Product: glutenin, high-molecular-weight
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPE
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F;22-838/Product:

glutenin, HMW chain #status predicted <MAT>

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A; Reference number: S36157
A; Accession: S36158
A; Molecule type: mRNA
A; Residues: 1-462 <RAB>
A; Cross-references: EMBL:X71427; NID:g395919; PIDN:CAA50558.1; PID:g4210364
C; Comment: This sequence is the chimeric product of a translocation mutation
C; Genetics:
A; Gene: GADD153/FUS
A; Map position: 12q13/16p11
A; Note: TLS is a synonym for GDB:FUS
C; Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Crozat, A.; Aman, P.; Mandahl, N.; Ron, D.

Nature 363, 640-644, 1993

N:Title: Fusion of CHOP to a novel RNA-binding protein in hum

A:Reference number: S33798; MUID:93288139

A:Accession: S33798

A:Accession: S33798

A:Molecule type: mRNA

A:Molecu
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A;Title: Fusion of the dominant negative transcription
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                                                                                                                                                          MNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGY 92
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                                                                                                                                                                                                                     Score 216; DB 4; Le
Pred. No. 9.2e-08;
Pred. No. 9.2e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:136048; OMIM:137070
A;Map position: 16p11.2-16p11.2
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A;Residues: 1-63,'S',66-526 <RAB>
A:Cross-references: EMBL:X71428;
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R;Crozat, A.; Aman, P.; Mano
Nature 363, 640-644, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rabbitts, T.H.; Forster, A.;
Nature Genet. 4, 175-180, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1.526 <CRO>
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 65; Conserv
                                       213 QSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQN 245
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                                                                                                                                                                                                                                                                                               33 MNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGY 92
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                                                                                                                                                                                                                                                     1 MASNDYTQQAT-----QSYGAYPTQPG-----
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                                                                                                                        GONYQHQQQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQQ 212
Q----QPSYGGQQQSYGQQQSYNPPQGYGQQN
                                                                                 SYGQQSSYPGYGQQPAPSS
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names: RNA-binding protein
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30.5%;
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Pred. No. 1e-07;
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US-09-219-849-34
US-09-219-849-34
US-09-219-849-391-2
US-09-390-200-2
US-08-328-809-8
PCT-US-258-442-13
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PCT-US-258-462-13
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US-08-556-9788-61
US-09-661-569-83-8
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US-09-661-800-8
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PCT-US93-03027-3
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US93/03027
FILING DATE: 1930401
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/862,987
FILING DATE: 06-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                             TELEPHONE: 212-758-48
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LEONARD,
APPLICANT: MICHEL
TITLE OF INVENTION:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: LEM PC COMPATIBLE
COMPUTER: LEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                HYPOTHETICAL: NO ORIGINAL SOURCE:
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                                                                                                                                       MOLECULE TYPE: pr
                                STRAIN: Oregon R
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                   TYPE: AMINO ACID
                                                                                                ORGANISM:
                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                        LENGTH:
                        HAPLOTYPE:
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US-09-034-177-3

US-08-538-711A-7

US-08-538-711A-7

US-08-725-027-7

US-08-725-027-7

US-08-705-660-26

US-08-965-903B-2

US-08-965-903B-2

US-08-477-346-29

US-08-477-346-29

US-08-477-346-29

US-08-447-348B-21

US-08-441-139-9

US-08-441-139-9

US-08-556-978B-21

US-09-247-806-4

US-08-687-702-37
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RELEVANT RESIDUES IN SEQ ID
PCT-US93-03027-3
                                                                                                                                                                                                                                                                                                            Patent No. 5750652
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 19,
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS,
TITLE OF INVENTION: ANTIBODIES, AND
                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                 NUMBER OF SEQUENCES:
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COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 NNNONSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSY 125
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                                                                                                                                                 ADDRESSEE:
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                                                                  10036-2711
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1987
                                                                                                                New York
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                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                Application US/08185432
                                                                                                                                E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steward,
                                                                                                                                                                                                                                                                               Artavanis-Tsakonas, Spyridor
Busseau, Isabelle
                                                                                                                                                                                                                                                              Diederich, Robert J.
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PC-DOS/MS-DOS
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Pred. No. 6.1e-10;
24; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                             Sequence 4, Applic Patent No. 5728810
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                 APPLICANT: Lewis, ....
APPLICANT: Xu, ming
APPLICANT: Xu, ming
APPLICANT: Hinman, michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2667 SPRSNSDWSEGVQSPAANN 2685
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                                                                                              CITY: Falls Church
STATE: Virginia
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                                                                        COUNTRY:
                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSPSTNMLSPSSQHNQQAFYQYLTPSSQHSGGHTPQHLVQTLDSYPTPSPESPGHWSSS 2666
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                                                                                                                                    3: Birch, Stewart, Kolasch & Birch 301 No. 5728810th Washington Street
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                                                                          U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08317844B Patent No. 5989894
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5999894th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GSAAAAAAAASGPGQQGPGGYGPGQQGPGGYGPGQ 237
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                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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APPLICATION
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Y: U.S.A.
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               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                           Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%; Score 163.5; DB 28.4%; Pred. No. 6e-07;
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In Release #1.0, Version #1.25
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Patent No. 5948640
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 241-1300
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               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mammalian Additional Sex NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 GSAAAAAAAASGPGQQGPGGYGPGQQGPGGYGPGQ 237
                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                STREET: 4560 Horto
CITY: Emeryville
STATE: California
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                                                                                   FILING DATE:
                                                                                                                                                                                                                      ZIP:
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REFERENCE/DOCKET NUMBER:
                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                 4560 Horton Street
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TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 923-3888

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-853-310-2
                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: amino acid sequence US-09-219-849-34
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US-09-219-849-34
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Best Local S
Matches 81
                 Query Match
Best Local Similarity
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 Matches
                                                                                                                                                                                                                                  SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                       APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULTABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                            LENGTH: 40
TYPE: PRT
                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQHQQQQNQQQHHQQLHIQDVVQLAQHSFMPQAHSEFGNDIGQEMLCDAVPMSAAEMEVS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKHQQI--QQFALQQAQLHQRQLLAQAANNNLLQQQQQQQQQ 354
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                                                                                                                                                                                                              401
   76;
                                                                                                                                                                                                                                                    PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           DE WOLF, FREDERIK A. MOOBROEK, ANDREAS WERTEN, MARC W.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAN HEERDE, GEORGE V.
VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
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 Conservative
                 11.6%; Score 156.5; DB 4; 27.1%; Pred. No. 1.5e-06;
 13;
Mismatches
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CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09247806 Patent No. 6280747 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.5%; Score 155.5; DB 4; Length 529; Best Local Similarity 27.7%; Pred. No. 2.7e-06; Matches 75; Conservative 12; Mismatches 105; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DEBMATOLOGICAL COMPOSITION CONTACTING
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
  205
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                                                                                                                          QQQGQQQQGHSSSFSALASMASSYLGNNSNSNSSYG-GQQQANEYGRPQHN------
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                                                                                                                                                                                                                     GNGGY-QQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQH 158
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                                                                                      -GPGQQGPSGPGSAAAAAAAAS----GPGQQGPGGYGPGQQGPGGYGPGQQGPSGPGSAA 204
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RESULT 8 US-08-749-391-2

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RESULT 9
US-09-200-2
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; Patent No. 6137032
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/749
FILING DATE: 13-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFFRENCE/DOCKET NUMBER: 93-9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
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amino acid
DGY: linear
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Selinger, Leonard B.
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Anaerobic Fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 150; DB 2; 28.4%; Pred. No. 7.4e-06;
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              RESULT 10
US-07-814-964-13
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 ; Sequence 13, Application US/07814964
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Best Local Similarity 28.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hu, Youji
APPLICANT: Forsberg, Cecil W.
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: A Xylanase Obtained From
TITLE OF INVENTION: Anaerobic Fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                         423
                                                                                                                                                                                           191 NSSYGGQQQANEYGRPQHNGQQQSNEYGRPQYGGNQNSN----GQHESFNFSGNFSQQNNN 247
                                                                                                                                                                                                                                                                    134 NQQQYNQ--QGQNNQQ-QYQQQGQNYQHQQQGQQQQQGHSSSFSALASMASSYLGNNSNS 190
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CITY: B
                                                                                                                           248 GNQ 250
                                                                                                                                                               363 GSPWGGNQGGNPWGGNQGGSPWGGNQGGSPWGQGNQGGNPWGGNQGGSPWGGNQGGNPWG 422
                                                                                                                                                                                                                                  306 NDQQGQQPPQGQQPPQGNDQQQGQQ-PPQPQGPQGGNPGGSDFNNWNQGGSPWGGN--QG 362
                                                                                                                                                                                                                                                                                                                                                                                  223 GNGNGGVSGTADFPYAKVYIGDGNGGGASPAPAGGAPAGGAPA-----
                                                                                                                                                                                                                                                                                                           269 QPQG-----PQGQQPPQGQQPPQGQQPPQGQQPPQGQQ-
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                           74 SQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQS 133
                                                                                                                                                                                                                                                                                                                                                                                                                    14 GQGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                         GNQ 425
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Selinger,
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Pred. No. 7.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07,
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 18-JUN-1990
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
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APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Spe
TITLE OF INVENTION: Protein and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION:
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                                   186 QRYYPNNMNALSSLLDPSSAGNAAGNANTATHPGLLPPNLQPQLTHHQQQMQQQLQLQQQ 245
148 QYQQQGQNYQHQQQGQQQQQ 167
                                                                                                                                                                      69
                                                                                                                                   64 -HSNNNQNSNNSQQGYNQSYQNGNQ------NSQGYNNQQYQGGNGGYQQQQGQ- 110
                                                                                                                                                                                                    37 NNNQQGQNQSSGGSSFGALASMAS----
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                                                                                                   ASSNNNSNNNNVSSGNNSTSSNPTQLAASQLNPATATTAAANN----AAGPASYLSQLPQV 185
                                                                  ----SGGAFSSL--ASMAQSYLGGGQTQS---
                                                                                                                                                                   SNSNNNVNVNALPQDFGYMQQTGSGQNYPTINQQQFSEFYNSFLSHLTQKQTNPSVTGTG 128
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Bruhn, Suzanne
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                                                                  -----NQQQYNQQGQNNQQ 147
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US-08-258-442-13
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ORIGINAL SOURCE:
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APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
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64 -HSNNNQNSNNSQQGYNQSYQNGNQ------NSQGYNNQQYQGGNGGYQQQQGQ-110
                                                69
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                                                                           37 NNNQQGQNQSSGGSSFGALASMAS----
                                                                                                                                                                         Local Similarity 26.2 los 68; Conservative
                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                            SNSNNNVNVNALPQDFGYMQQTGSGQNYPTINQQQFSEFYNSFLSHLTQKQTNPSVTGTG 128
                                                                                                        QQQQQQQQQQQQQQAPYQGHFQQSPQQQQQNVYFPLPPQSLTQPTSQSQQQQQQQXANSN 68
                                                                                                                                         QGQGQGQGQGQGQGQGSF------TALASLAS-----SFMNSN 36
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Bruhn, Suzanne
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                                                                                                                                                                      Score 145; DB 1; Pred. No. 2.4e-05;
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                                                                               -SFM----
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ASSNNNSNNNVSSGNNSTSSNPTQLAASQLNPATATTAAANN---AAGPASYLSQLPQV 185

186 QRYYPNNMNALSSLLDPSSAGNAAGNANTATHPGLLPPNLQPQLTHHQQQMQQQLQLQQQ 245

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Ouery Match Ouery Match Best Local Similarity 26.2%; Pred. No. 2.4e-05; Matches 68; Conservative 15; Mismatches 81; Indels 96; Gaps 9; Oy 1 ogogogogogogogogosp	RESULT 12 US-08-328-809-8 US-08-328-809-8 Sequence 8. Application US/08328809 Patent No. \$70334 APPLICANT: Lindbran, John M. APPLICANT: Essigmann, John M. APPLICANT: Essigmann, John M. APPLICANT: Brown, Steven CORRESPONDENCE NODERS: APPLICANT: Brown, Steven CORRESPONDENCE NODERS: ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibeault STREET: 53 State Street CITY: Boston ZIF: 02109 COMPUTER READMLE FORM: COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: GRAPHICATION COUNTRY: USA COUN	Qy 148 QYQQQGQNYQHQQQGQQQQ 167
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PCT-US92-11107-13
                                                                                               ; CLONE: fractional yeast SSRP (fysSRP) (predicted) PCT-US92-11107-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application PC/TUS9211107 GENERAL INFORMATION:
Query Match 10.8%; Score 145; DB 5; Best Local Similarity 26.2%; Pred. No. 2.4e-05; Matches 68; Conservative 15; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
                                                                                                                                                                                                                                                                                                          FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Grannahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                        TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Sac
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 542 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19921218
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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CITY: L
STATE:
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                                                                                                                                                                                                               LENGTH: 542 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
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                                                                                                                                                         Saccharomyces cerevisiae
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25
                                     Length 542;
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     Indels
       96;
     Gaps
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RESULT 15
US-08-556-978B-59
; Sequence 59, Application US/08556978B
; Patent No. 6268169
; Patent No. 6268169
; GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRO
TITLE OF TOPENTION: SPIDER SILK ANALOGS
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US-09-625-188-20
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US-09-625-188-20
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SEQ ID NO 20
LENGTH: 729
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Best Local Similarity 25.2
Matches 62; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                  458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GQGQGSFTALASLASSFMNSNNN--NQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNN 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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                                           PRODUCED
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/077,60
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROSOFT WORD FOR WINDOWS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100.
CITY: WILMINTON
STATE: DELAWARE
TOWNEY: UNITED STATES OF AMERICA
                                                                                                                                 110
                                                                                               160 QQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYG-GQQQANEYGRPQHN------
                                                                                                                                                              101 NGGY-QQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQ 159
                                                                                                                                                                                                64 GQGQQGPSGPGSAAAASAAAS------AESGGPGGYGPGQQGPGGYGPGQQ--G
                                                                                                                                                                                                                              51 SFG-----ALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGG 100
                                                                                                                                                                                                                                                               14 GYGPGQ-QGPGRYGPGQQGPSGPGSAAAAAA------GSGQQGPGGYGPRQQGPGGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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AAAAGPGQQGPGGYGPGQQG
                                                                GPGQQGPSGPGSAAAAAAAAAS----GPGQQGPGGYGPGQQGPGGYGPGQQGTSGPGSAAA
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                                -----GQQQSNEYGRPQYG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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1007 MARKET STREET
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                                                                                                                                                                                                                                                                                                                                               Score 142.5; DB 4
Pred. No. 3.5e-05;
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Gaps

15;

50

109

209 154

Search completed: February Job time: 237 sec

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2002, 15:02:17

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Result
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Copyright (c) 1993 - 2000 Compugen
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with self-assembly reatment of prion diseases, s	șr N, Scheibei T;	Cabalba						yene therapy; on disease.	enic protein.			<b>-</b>		sequ apop	Amphiphilic recomb Plasmodium falcipa	Polar gelatin P te Amphiphilic recomb	Human additional s	Huntingtin accumul	Sequence deduced F	Ď,	Nephila clavipes s	ipes	acid	Amino acid sequenc	ce of	Arabidopsis Chara		0	Arabidopsis thalia	σ.	untingtin	C albicans apoptos Apo-lipoprotein E	icotiana p

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Matches 253
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                                                                                                                                                                                              SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease.
 Lindquist
                                                         09-JUN-1999;
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                                                                                                                                                                                                                                                       sequence of a putative prion protein.
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Best Matches 253; Query Match

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AAB30821-23 represent putative prion proteins which have been CC identified from a yeast protein database. The specification describes chimeric polypeptides, which comprise at least one SCHAG (self-CC coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker CC protein, a glutathione-S-transferase or a staphylococcal nuclear CC protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        properties,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also related aggregates, fibrils and polymers
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23-JUN-1988;

88WO-US02129

29-DEC-1988.

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Best Local Similarity
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      Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp -
                                                        WPI; 2000-679800/66
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                                                                                                                                                                                                                           Ruminococcus flavefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF lies between the FUS 1 or BIK 1 promoter, BIK At least one polypeptide may be promoted within a induced by a factor for alpha cells, alpha-factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 4; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA fragment contg. protein encoding gene and yeast promoter controlled by mating pheromone allowing efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fink GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1987;
                                                                                                      (XENC-) XENCOR INC
                                                                                                                              12-MAY-1999;
                                                                                                                                                     12-MAY-2000;
                                                                                                                                                                             16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulatable expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                             121 MAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QGQGQGQGQGQGQGQGQGGSFTALASLASSEMNSNNNNQQGQNQSSGGSSFGALASMAS 60
                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qgqgqgqgqgqgqgqgqgsftalasltssfmnsnnnnqqgqnqssggssfgalasmas 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1989-023850/03
DB; AAN93100.
                                                                                                                                                                                                                                                                                                                                                                                                                    maqsylgggqtqsnqqqynqqgqnnqqqqqqqqqhs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGGSGGAFSSLAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stmhsnnnqnsnnsqqgynqsyqngnqnsqgynnqqyqggnggyqqqqqqgqsggatsslas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHITEHEAD INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trueheart J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                     2000WO-US13172
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                             99US-0133714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87US-0066078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 895; DB 10;
Pred. No. 5.5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EA;
                                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 running 3' to 5'.
high-copy vector
for a-cells using this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
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RESULT
AAR75506
ID AAR7
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     FTT FXX X X X X E
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 16S;
              Misc-difference
                                                                                                                                                                                                  Nicotiana
                                                                                                                                                                                                                                                               Nicotiana alata
                                                                                                                                                                                                                                                                                        05-DEC-1995
                                                                                                                                                                                                                                                                                                                AAR75506;
                                                                                                                                                                                                                                                                                                                                         AAR75506 standard;
                                                              Misc-difference
                                                                                      Misc-difference
                                                                                                              Misc-difference
                                                                                                                                     Peptide
                                                                                                                                                                         Key
                                                                                                                                                                                                                           adhesive.
                                                                                                                                                                                                                                      Arabinogalactan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the active compound in a bleaching agent which is used for bleaching
                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                     513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 YQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQ-QQYNQQGQNNQQQYQQQGGQNYQHQQQG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ndwnnwg----qqnndwnqwnnqn-nnqqnawngwdnnnnwnqnnqqqnnwdwnnqnnwn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                     573 nwngw 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggqqqnndwnnwgqqnndwnqwnnqgqqqnndw-----nhwgqqnndwnqwnnqgqqqn 360
                                                                                                                                                                                                                                                                                                                                                                                                                             NQNRY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     nggnndwngynnggggnndwngwnngnnngwngwnngnngnnnggnawngwdnnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQQANEYGRPQHNGQQQSNEYGRPQYGGNQNSNG--QHESFNFSGNFSQQN-----NNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qqnawngwdnnnnwnqwdqnnqwnnqqq-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nngqqnndwngwnn-----qnnwnnngqqnndwngwnnggqqnndwngwnngnnwngnnn 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGSSFGALASMASSFMHSNNNONSNNSQQGYN--QSYQNGNQNSQGYNNQQYQG-GNGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
80; Conser
                                                                                                                                                                                                  alata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     954 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                        (first entry)
              /note=
38
                                                                                      /note-
37
                                                                                                            /note-
26
                                     /note=
26..36
                                                                                                                                                                                                                                                              arabinogalactan protein NaAGP1
                                                                                                                                     /label= signal 26..40
                                                                                                                                                                                                                                      protein;
                                                                                                                                                                        Location/Qualifiers
 /note=
                                                                         note-
                                                                                                                                                                                                                                                                                                                                        Protein; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114pp; English
                                                                                               "Ala
                                                                         "His in
"microsequenced and
                        "microsequenced derived
                                                 "X in peptide"
                                                                                                                        "corresp. to microsequenced
                                                                                                                                                                                                                                      AGP; gum; thickening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                               in peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 218;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QQQGHSSSFSALASMASSYLGNNS---NSNSSYGG
                                                                        peptide"
                                                                                                                                                                                                                                                                                                                                         Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
derived SQ identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                     agent; emulsifier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQs identical*
                                                                                                                                                                                                                                                               encoded by cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----nntwdwnngnnwnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 954;
                                                                                                                        peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
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RESULT
AAB63197
ID AAB6
XX
AC AAB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from N. alata suspension culture. It was used as a template for the synthesis of an oligo primer which was further utilised for the isolation of a hybridising AGP gene from both N. alata and N. plumbaginafolia. Degenerate reverse primers corresp. to part of the AGP N-terminal AA sequence were synthesised and used to obtain a 160 bp primer extension product, which was then amplified by PCR. Additional primers, corresp. in sequence to parts of the 160-bp fragment were synthesised and used to amplify the 3' part of the AGP gene by nested PCR. The primers were AAQ92536 and AAQ92537. A 1.6 kb fragment was amplified and sequenced. The alignment of the sequences obtd. from the two PCR reactions gave rise to a DNA sequence shown. The PCR fragment encodes a groterise to a DNA is periode (AAR75513) by protein sequencing with two mismatches the PCR sequences after the AAQ92524 FT). The 1.6 kb PCR fragment was used to screen a cDNA library made from RNA isolated from N. alata cells. The alignment of the PCR sequences with the cDNA sequence gave rise to aAQ92524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
       AAB63197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant plant arabinogalactan protein and cloned DNA encoding it useful as an emulsifying agent, adhesive agent or a lubricating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-1994;
03-DEC-1993;
                                                          AAB63197 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The N-terminal region of an arabinogalactan protein (AGP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacic A, Chen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09515377-A
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                                                                                                                                                                                                                                          193
                                                                                                                                                                                                                                                                                            315
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                                                                                                                                                                                                                                                                                                                                                                                              255
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                                                                                                                                                                                                                                                                                                                                                                                                                                              88
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4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the PCR sequences with the cDNA sequence gave rise to AAQ92524 e calc. mol. wt. of the encoded protein is 51.8 kD with a
                                                                                                             σ
                                                                                                                                                                                       V---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSNNNNQQG--QNQSSGGSSFGALASMASSFMHSNNNQNSN----NSQQGYNQSYQNGNQ
                                                                                                                                                                                                                                  SYGGQQQANEYGRPQHNGQQQ----SNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGN
                                                                                                                                                                                                                                                                                    senynnnnnnvfsenynnnnnnafyenynnnnngyseny----nqassy---nnndnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nnnnnnddgfsenynnngysenannknnngysenynnnnnngyaknynngysqsynnnnn
                                                                                                                                                                                                                                                                                                                                    QQQYNQQGQNN--QQQYQQQGQNYQHQQQGQQQQGHSSSFSALASMASSYLGNNSNSNS
                                                                                                                                                                                                                                                                                                                                                                                      fysenynnnnnnvfsensnnngyskkinnngysqnymnnnngfsesynnnnnnnnnnnvf
                                                                                                                                                                                                                                                                                                                                                                                                                                      -NSQGYNNQ----QYQGGNGGYQQQ---QGQSGGAFSSLASMAQSYLGGGQTQSN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Figure 1F; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 27.156; Conservative
                                                                                                                                                                                  erqglsdtrflengkyyyd1kne----ntnnngysenyn---hvssynnnnn
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93US-0161944.
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                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.1%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 203.5; DB 16; pred. No. 2.8e-09; 33; Mismatches 96;
                                                          280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                                       367
                                                                                                                                                                                                                                                                                                                                       192
                                                                                                                                                                                                                                                                                                                                                                                         314
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7 QGQGQGQGQGQGGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMASSFMHSN

Best Local Similarity Matches 69; Conserv

Conservative

32;

Mismatches 104;

Indels 53; Length

Gaps

9;

66

14.78; 26.78;

Score 198.5; DB 2 Pred. No. 4.1e-09;

DB 21;

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fungicide; and ophthalmological. The polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin againg due to sunburn, to maintain organs before transplantation, for
                                                     supporting cell culture of primary tissues, to regenerate tissues and chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, AAF2364 to AAF2372 and AAB63133 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                         and polypeptides homologous to them. Human secreted proteins have activities based on the tissues and cells the genes are expressed Examples of activities include: immunosuppressive; antiarthritic;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 500-501; 533pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000WO-US09071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis; nervous system disorder; Alzheimer's
ocular disorder; corneal infection; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AAB63182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM, Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1999;
20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001 (first entry)
                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; diagnosis; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF22421 encode the human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB63183 to AAB63231 represent more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0128694.
2000US-0176931.
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                                                                                                                                                                                                                                                                                                                                                                                                      DNA binding region of which may be mutated by replacing one or more amino acids. This allows inhibition, prevention or control of DNA binding and thus activation of genes controlled by the protein can be controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPI;
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                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27-29; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutation of DNA binding region of NF-KB/rel/dorsal protein \cdot to prevent or control binding to DNA for control of gene activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leonard WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-KappaB/Rel/Dorsal; NRD; DNA binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR42087 standard; protein; 678
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                                                                                                                                                                                                                    Score 198; DB 14;
Pred. No. 1.3e-08;
4; Mismatches 76;
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                                                                                                                                                                                                                                                                     Length 678;
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                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    schizophrenia; dopamine; cAMP; adenosine; thromi muscarinic acetylcholine; endothelin; bombesin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor; ligand binding assay; transmembrane schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The peptides AAW03578-W03651 represent the N-terminal fragments of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dopamine receptor peptide - useful as antipsychotic agent, treating schizophrenia
NGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGRPQH--NGQQQSNEYGRPQY-----GGNQNSNGQHESFNFSGNFSQQNNNG 248
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                                                                ALASLASSEMNSNNNNQQGQNQSSGGSSEGALASMASSEMHSNNNQNSNNSQQGYNQSYQ 83
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                                                                                                                                                                                                                                                                                                                                                                                342 AA;
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schuster
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92US-0943236.
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                                                                                                                                                                                                                                        Score 192; DB 17;
Pred. No. 1.8e-08;
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                                                                  Query Match
Best Local :
                                                       Matches
                                                                                                                                                The present invention describes a method for inhibiting the formation aggregates of certain proteins, involving contacting the protein with binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's an Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                      Disclosure; Page 100; 108pp; English.
                                                                                                                                                                                                                                                                                                               Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                                                                                                Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1999; 99US-0146047
21-JUL-2000; 2000US-0620955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                          (MESS/) MESSER A. (LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MESS/) MESSER A.
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gggggkgpvtgtgsmatleklmkafeslksfqqqqqq---
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                                                     Conservative
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                                                                  14.1%;
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                                                   Score 189.5; DB 22
Pred. No. 1.1e-08;
9; Mismatches 69;
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                                                                              22;
                                                     Indels
                                                                              Length
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                                                    Gaps
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Query Match Best Local S Matches 72

Similarity 72; Conserv

Conservative

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13.9%;

Score 187.5; DB 22; Pred. No. 1.3e-07; 3; Mismatches 125;

Indels Length

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                             The present invention provides the protein and coding sequences of two human nuclear factors associated with dsRNA (NFAR-1 and NFAR-2). These are transcriptional regulators and aire thought to play a role in apoptosis and tumourigenesis. The coding sequence (found on chromosome 19p13.1-13.2) is useful as a probe to detect rearrangements in tumour cells and the protein is useful for determining structure-function
                                                                                                                                      Novel isolated human nuclear factor associated with dsRNA polypeptide useful for determining structure-function relationships and as affining to identify and isolate interacting proteins that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35148 standard;
Sequence
                    relationships.
                                                                                                        Claim
                                                                                                                                                                                  N-PSDB; AAC67269
                                                                                                                                                                                                                Barber GN,
                                                                                                                                                                                                                                    (BARB/) BARBER G
(SAUN/) SAUNDERS
(PERK/) PERKINS I
                                                                                                                                                                                                                                                                               11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                           21-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         tumourigenesis
                                                                                                                                                                                                                                                                                                                                                                                                 Human; nuclear factor associated with dsRNA; NFAR-1; NFAR-2; transcription regulator; chromosome 19p13.1-13.2; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGQTQSNQQQYNQQGQNNQQQQQQQQQQQQQQQQGGHSSSFSALASMASSYLGNN
                                                                                                                                                                                             2001-080688/09
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894
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                                                          amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable
                                                                                                                                                                                               The present sequence represents a modified N region of Sup35 protein, in the second oligopeptide repeat has been expanded twice, creating a total of seven repeats. Sup35 possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of Sup35 in a manner that creates a heritable change in phenotype. It is used to construct chimeric polypeptides of the invention, which comprise at least one SCHAG (self-coalesces into higher-order aggregates)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
              pigmentation
                          chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant
                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li L,
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               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHAG; self-coalesce; higher-order aggregate; ain; aggregation; fibril; phenotypic alteration; ease resistance; plant pigmentation; prion disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma
              diagnosis
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                                                                                                                                                                                                                                                                                                                                                                          fibrils and polymers
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              and
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            treatment of
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                                                                                                                                                                                                                                                                                                                                                             Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75507 standard; Protein; 437
Bacic A,
                                       18-JUL-1994;
03-DEC-1993;
                                                                                                                                            Misc-difference
                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana
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                                                                      01-DEC-1994;
                                                                                          08-JUN-1995
                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                              Peptide
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                    (ALBR ) ALBRIGHT & WILSON AUSTRALIA.
                                                                                                             W09515377-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSYLGNNSNSNSSYGGQQQANEYGRPQHNGQQQSNEYGRPQYGGNQNSNGQHESFNFSG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sdsnqgnnqqnyqqysqngnqqqgnnryqgyqaynaqaqpaggyyqnyqgysg-----
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63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                              plumbaginafolia arabinogalactan protein NpAGP1
 Chen
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93US-0161944.
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14..24
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                                                                                                                                  /note-
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                                                                                                                                                                          /label= see
                                                                                                                                                                                             'label=
                                                                                                                                                                                                                 'label= hydroxyproline
                                                                                                                                                                                                                                      'note-
                                                                                                                                                                                                                                                         note-
                                                                                                                                                      label- see above
 Clarke AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.7%;
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                                                                                                                                                                                                                                      "see above"
                                                                                                                                                                                                                                                                              "see
                                                                                                                                                                                                                                                                                                "identical with microsequenced peptide"
                                                                                                                                                                                                                                                          "see above'
                                                                                                                                                                                                                                                                                                                    "corresp. to microsequenced peptide"
                                                                                                                                                                                              see
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                                                                                                                                                                          above
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Pred. No. 5.8
 Du H,
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RESULT 1
AAG70847
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AC AAG7
XC AAG7
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DT 27-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 bp primer extension product, which was then amplified by PCR.

Additional primers, corresp. in sequence to parts of the 160-bp

C fragment were synthesised and used to amplify the 3' part of the

CAP gene by nested PCR. The primers were AA092536 and AA092537. A

1.6 kb fragment was amplified and sequenced. The alignment of the

Sequences obtd. from the two PCR reactions gave rise to a DNA

sequences obtd. from the two PCR reactions gave rise to a DNA

sequences shown. The PCR fragment encodes a protein conty.

the peptide (AAR75513) by protein sequencing with two mismatches

(see AA092524 FT). The 1.6 kb PCR fragment was used to screen a cDNA

ilbrary made from RNA isolated from N. alata cells. The alignment

of the PCR sequences with the cDNA sequence gave rise to AA092524.

The calc. mol. wt. of the encoded protein is 51.8 kD with a

predicted pI of 3.84. An N. plumbaginafolia cells suspension cDNA

ibrary was also screened with the PCR fragment. The AAP gene was

designated NPAGP1 (see AAQ92525). The NPAGP1 was not identical but

very similar to the NBAGP1 at both the nt. and the derived AA

level It contains hydroxyproline residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                          C albicans apoptosis associated protein #27
Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration.
                                                                                                   27-JUL-2001
                                                                                                                                                                                AAG70847 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The N-terminal region of an arabinogalactan protein (AGP) was obtd. from N. alata suspension culture. It was used as a template for the synthesis of an oligo primer which was further utilised for the isolation of a hybridising AGP gene from both N. alata and N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant plant arabinogalactan protein and cloned DNA encoding it useful as an emulsifying agent, adhesive agent or a lubricating agent.
                                                                                                                                           AAG70847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                     216 EYGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGN 249
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                                                                                                                                                                                                                                                                                                                                                            nn-----nnnnnvfs-----enynnnnnafsenynnnnvfsenynknnnnafse
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                                                                                                                                                                                                                                                                                                                                                                                                                                           kkinnngysqnymnnnngfs-----esy----nsnnnnnifsenynnnnnnvfseny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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23.4%; Pred. No. 1e-(
tive 37; Mismatches
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No. 1e-07;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identitreatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaen and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
                            Protein
                                       Key
                                                                  Synthetic
                                                                                             androgen;
                                                                                                           Apo-lipoprotein E; cell differentiation; hypercholestrolaemia
                                                                                                                                     Apo-lipoprotein E induced cell differentiation copying polypeptide
                                                                                                                                                                 17-MAY-1991
                                                                                                                                                                                            AAR11019
                                                                                                                                                                                                                     AAR11019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2;
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N-PSDB; AAH29883.
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                                                                                                                                                                                                                                                                                        678
                                                                                                                                                                                                                                                                                                                136 QOYNQQGQNNQQQYQQQGQNYQHQQQQQQQQQGHSSSFSALASMASSYLGN 186
                                                                                                                                                                                                                                                                                                                                           640 ngynpkngyynnnsknlsnn--fglngmhgqng-----
                                                                                                                                                                                                                                                                                                                                                                                              589 aaatasgqplnlnnnaflnlqqqqsqsqpqgqhhyn-----qhsrnnnasgaskfn 639
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                                                                                                                                                                                                                                                                                                                                                                                                                          24 ALASLASSEMNSNNN-----NQQGQNQSSGGSSEGALASMASSEMHSNNNQNSNNSQ--
                                                                                                                                                                                                                                                                                                                                                                      QGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQ 135
                                                                                                                                                                                                                                                                                     \tt qqlqqqqqqqqqqqqqqqqqqqqqqqqqdhdlngsssshqsklqlnn
                                                                                                                                                                                                                     standard; Protein; 590
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                                                                                              diagnosis
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218pp; English.
/label= leader_segment
/note= "may be replaced by NH2'
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 184.5; DB 2
Pred. No. 1.8e-07;
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26-FEB-1990;
18-JUN-1990;
                                                                                                                                                                                                                                                                                                         A polypeptide capable of inhibiting lymphocyte proliferation and/or ovarian androgen secretion comprises a plurality of segments, as indicated in the features. The segment may be repeated 2-10 times. In this example the segment is repeated 10 times. The N-terminal may comprise NH2 or a leader segment of 1-20 amino acids, the C-terminal comprises COOH or a tail segment of 1-20 amino acids. Between each segment is a first and second spacing segment of 1-20 amino acids. p(141-155) is a peptide obtained from apo E. see also AARII107 and AARII109.
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 98; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide(s) copying apo-lipoprotein E induced cell differentiation - useful for treating hypercholestrolaemia, inhibiting ovarian androgen secretion and for prodn. of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-087246/12.
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                                                                                                          QQQGQNYQHQQQGQQQQGHSSSFSALASMA---SSYLGNNSNSNSSYGGQQQANEYGRP
                                                                                                                                  QGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNNQQQY 149
                                                                                                                                                                               NSNNNNQQGQNQSSGGSSFGALASM----ASSFMHSNNNQNSNNSQQGYNQSYQNGNQNS 89
                                         SCRIPPS CLINIC & RE.
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90US-0485158.
90US-0540363.
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41..55
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/label= first_spacing_segment
/note= "may be omitted"
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21..130
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                                                                                                                                                                                                                           Score 183.5; DB 12;
Pred. No. 1.7e-07;
2; Mismatches 124;
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                                                               -----POYGGNONSNGOHESFNFSGNFSOONNNGN 249
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Search completed: Job time: 256 sec

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                                                                                                                                                                                                                                                                                                                                                 aggregates of certain proteins, involving contacting the protein with binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurological disorder; Huntington's disease; Alzheimer's disease; Parkinson's disease; prion disease; frontôtemporal dementla; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1 SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabod
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 99; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-1999; 99US-0146047
21-JUL-2000; 2000US-0620955
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(MESS/) MESSER A.
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                                                                                    MAQSYLGGGQTQSNQQQYNQQGQNNQQQYQQQGQNYQHQQQGQQQQQGHSSSFSALASMA 180
                           SSYLGNNSNSNSSYGGOOOANEYGRPOHNGOOOSNEYGRPOYGGNONSNGOHE 233
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS	Q9UVK9	Q9TY17	Q9TYH5	Q20497	Q94464	_	റ	_	0		_	_	_		o	_	o		Q9BXC6	0	3 Q91551		_		Q27512	
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	YKNENYNNNLQGYQAGEQPQ 120	PAGGYYQNYQGYSGYQQGGY 60	3; Length 685; 61; 0; Indels 0; Gaps	54 CRC64;				TOR FAMILY	5 gene.";		•		Saccharomyces.			pour co,	ate)	_			

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SGD; S0002579; SUP35.
Interpro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
GTP-binding; Protein biosynthesis.
SEQUENCE 224 AA; 25182 MW; 2521.
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01-MAR-2001
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POLYPEPTIDE 1
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007089;
01-NOV-1996
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01-JUN-2001
                        Nakayashiki T., Ebihara K., Nakamura Y.;
"PSI-like properties of fungus Sup35 proteins.";
Submitted (MAR-2000) to the EMBL/GenBack/DDBJ databases.
-- SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AB039750; BAB12661.2;
InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                        Candida maltosa (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                           SUP35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88329727; PubMed-3047009; Kushnirov V.V., Ter-Avanesyan M.D., Smirnov V.N., Inge-Vechtomov S.G.; "Nucleotide sequence of the SUP2 (SI cerevisiae."; Gene 66:45-54(1988).
        PRINTS;
                                                                                                                                                        SEQUENCE FROM N.A. Nakayashiki T., Eb
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacciaromycetales; Saccharomycetaceae; Saccharomyces
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annotation update)
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hes 0;
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Matches 57
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Best Local :
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL; AF206287; AAF14002.1; -
NON TER 299 29
SEQUENCE 299 AA; 32702 Mar.
                                                 01-MAY-2000
01-MAY-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UVK3;
Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding; Protein biosynthesis. SEQUENCE 712 AA; 78631 MW; 729B6A814735C469 CRC64;
                               SUP35
                                          SUP35
                                                                                            Q9URS3
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; /
Saccharomycetales;
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                                                                                                                                           GYQQYNSQPQQQ
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                                                                                                                                                                                    QQQYGGYNQYNQYQGGYQQNYNNRGGYQQGYNNRGGYQQNYN---NRGGYQGYNQNQQYG
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                                        HOMOLOG
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                                         (FRAGMENT).
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mitosporic
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Last annotation updat
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Pred. No. 6.2e-15
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Pred. No. 1.1
 Saccharomycotina; Saccharomycetes; cetaceae; Kluyveromyces.
                                                                                           PRT;
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annotation
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on update)
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                                                                                                                                                                                                                                                                                       Length 299
                                                                                                                                                                                                                                                                                                                       CRC64
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Matches 62
                                                                                                                                                             Query Match
Best Local Similarity
Matches 62; Conser
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Q9HGI8;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                         Nakayashiki T., Ebihara K., Nakamura Y.;
"PSI-11ke properties of fungus Sup35 proteins.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AB039749; BAB12680.1; -.
InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNECT.
GTP-binding; Protein biosynthesis.
SEQUENCE 700 AA; 77639 MW; 53F9905442F6B025 CRC64;
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PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding; Protein biosynthesis.
NON_TER
428
428
428
428
47156 MW; 842
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Molecular Basis of a Yeast Prion Species Barrier.";

Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databa-
1- SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAM
EMBL; AF206288; AAF14003.1; -.

HSSP; P07157; 1AIP.
InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
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                                                                                                     MSD-SNQGNNQ-QNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQG
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                                       GYQQYNPDAGYQQYNPQGGYQQYNPQGGYQQQFN-PQGGRGNYKNFNYNN------NL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYQGYNPQQA--QGYQP---
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AYQGYNPQQA--QGYQP---YQGYNAQ---QQGYNAQQGGHNNNYNKNYNNKNSYNNYNK 110
                                                                              MSDQQNQDQGQGYNQYNQYGQYNQYYNQ-QGYQGYNGQ-QGAPQGYQAYQAYGQQPQG
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62; Conserv
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1 (TrEMBLrel. 16,
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E RELEASE FACTOR:
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47
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. 16, Last sequence. 17, Last annotation.
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Last annotation update)
                                                                                                                                                           Score 212; DB
Pred. No. 5.4e
4; Mismatches
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Pred. No. 3.3e-13;
4; Mismatches 44
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cetaceae; Kluyveromyces
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Q9UVK2
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Best Local S
Matches 63
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submitted (NOV-1999) to the EMBL,
-: SIMILARITY: TO GTP-BINDING EI
EMBL; AF206289; AAF1404.1; --
InterPro: IPR000795; GTP_EFTU.
Pfam: PF00009; GTP_EFTU; 1
                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Nakayashiki T., Ebihara K., Nakamura Y.;

Nakayashiki T., Ebihara K., Nakamura Y.;

"PSI-like properties of fungus Sup35 proteins.";

"PSI-like properties of fungus Sup35 proteins.";

"BII-like properties of fungus Sup35 proteins.";

"BII-like properties of fungus Sup35 proteins.";

"STATIARITY: TO GTP-BINDING ELONGATION FACTOR
                                                                                                                                                                                                                                                                                                                     01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9UVK2 PRELIMINARY; PRT; 320 AA.
09UVK2; PRELIMINARY; PRT; 320 AA.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUP35
                                   -!- SIMILARITY: TO GTP-BINDING EMBL; AB039751; BAB12682.2; -. InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                 Debaryomyces hansenii (Yeast) (Torulası
Eukaryota; Fungi; Ascomycota; Saccharor
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                            Q9HGI6;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces marxianus (Yeast) (Kluyveromyces fragilis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                      Q9HGI6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP-binding; Protein biosynthesis NON_TER 320 320
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  PRINTS;
                      Ptam;
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                                                                                                                                                                                                 NCBI_TaxID=4959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGYKVLKDXXXXXXXXXXAPAQSSSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFN-PQGGRGNYKNFNYNN------NL
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                      PF00009;
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  PR00315;
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(TrembLrel. 17, La
(TrembLrel. 17, La
RELEASE FACTOR 3.
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                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                    GTP_
  ELONGATNECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
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                      EFTU;
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Yeast Prion Species Barrier.";
to the EMBL/GenBank/DDBJ databases.
P-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGFQPQSQG
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Last annotation update)
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Pred. No. 1.5e-
5; Mismatches
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Saccharomycotina Sacc
cetaceae; Debaryomyces.
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-QGAPQGYQAYQAYGQQPQG

58 58 Length 320

Indels

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Best Local S
Matches 60
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01-MAR-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakayashiki T., Ebihara K., Nakamura Y.;
"PSI-like properties of fungus Sup35 proteins.
submitted (MAR-2000) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: TO GTP-BINDING ELONGATION FACT
EMBL; AB039753; BAB12684.2;
InterPro; IPR000795; GTP_EFTU.
                     Q9UVJ9;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
       SUP35
                                                                                                     Q9UVJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00315; ELONGATURECT.
GTP-binding; Protein biosynthesis.
SEQUENCE 662 AA; 73780 MW; 2641046199FB1E04 CRC64;
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Eukaryota; Fungi;
Saccharomycetales;
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SEQUENCE 701 AA; 77227 MW; 375172E34289F554 CRC64;
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                                                                                                                                                                                                                                   PQSQ 122
                                                                                                                                                                                                                                                                                                                                               MSDPNQ-NGQ------QGGQQNAGGNYYQQYFQKLTQQAQ-AGGGYQPYGGYGGY--GG
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         HOMOLOG
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58; Conservative
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(TremBLrel. 17, Last seq
(TremBLrel. 17, Last ann
RELEASE FACTOR 3.
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                                                                                                     PRELIMINARY;
       (FRAGMENT).
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Ascomycota; Saccharomycotina; Saccharomycetaceae; Zygosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                        27.1%;
46.8%;
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38.5%;
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                         Last sequence update)
Last annotation updat
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Pred. No. 2.8e
8; Mismatches
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Pred. No. 7.2e-11;
1; Mismatches 39
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2.8e-11;
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CTOR FAMILY.
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Q9HGI5
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Best Local
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Best Local 9
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Nakayashiki T., Ebihara K., Naka
"PSI-like properties of fungus S
Submitted (MAR 2000) to the EMBL
-i- SIMILARITY: TO GTP-BINDING E
EMBL; AB039752; BAB12683.1; -
InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; I.
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.01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                 PRINTS; PR00315; ELONGATNFCT.
GTP-binding; Protein biosynthesis.
SEQUENCE 742 AA; 80125 MW; 3C8D3F5738206C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HGI5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular Basis of a Yeast Prion Species Barrier.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
'! SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AF206292; AAF14007.1;
InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zygosaccharomyces rouxii (Candida mogii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HGI5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUP35
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                                                                                               1 MSDS-NQG-NNQQNYQQYSQ-NGNQQQGNNRYQGYQAYNAQAQ
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     ---PAGGYYQNYQGYSGYQ-
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                                                            MSDQFNQDFANKANINEQGQGQGQGQGG----QGYGQYQAPQQFVPGQSFVPGQSFVPGQ
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                                                                                                                                                       Similarity
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1 (TrEMBLrel. 16, 1
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E RELEASE FACTOR 3
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                                                                                                                                        Conservative
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                                                                                                                                                         25.0%;
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                                                                                                                                                                                                                                                                                                                                                                K., Nakamura Y.;
fungus Sup35 proteins
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence up
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Pred. No. 5.4e-10;
3; Mismatches 32
                                                                                                                                                         Score 175; DB 3; Pred. No. 2.4e-09;
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                         QGGYQQYNP-----
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                                                                                                                                        Mismatches
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DAGYQQQYNP

58;

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: Gaps

56 40 Indels

34;

Gaps

10;

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SFAPQGGYDQ-YQGQGGYQGGYQGGYQGNNRGGYSGRGRGGYRGGYQGGYNNQYGN

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Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Ra Alzawa K., Kasha M., Yamanaka I.,

Ra Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole Bonaldo M.F.,

Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Ra Mordone P., Ring B., Ringwald M., Jamazzarelli J., Sakamoto N.,

Ra Alyasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ra Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ra Alyasaki Y., Storch K., Schoenbach C., Seya T., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 49
      Q9UVKO;
Q9UVKO;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085680; PubMed=11217851;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
2610111C21RIK PROTEIN.
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EMBL; AK011843; BAB27875.1; -.
MGD; MGI:1917689; 2610111C21Rik.
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                                                                                                                                                                                                                                                                         QSGYDQH--QGSYDEQSNYQ-----QHDSYNQNQQSYHS 149
                                                                                                                                                                                                                                                                                                                                                                                          QNQSGYSQSYGSYENQKQSSYGQQSYNNQGQQNTESSGGQGGRAPSYGQSDYGQQDSYDQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSDSGSYSQSGGEQQSYSSYGNQGSQGYGQTP-QGYSGYGQTTD--SSYGQNYGGYSGYG
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                                                                                                                          PRELIMINARY;
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Rodentia;
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Last annotation updat
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.9e-09;
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, Fukuda S.,
Yamanaka I.,
., Saito R.,
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Best Local Similarity
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Best Local :
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Q9B119;
01-JUN-2001
01-JUN-2001
01-JUN-2001
GRAAL2 PROTE
                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
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"Molecular Basis of a Yeast Prion Species Barrier.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AF206291; AAF14006.1;
-- Interpro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Graal a Drosophila gene coding for several mosaic seri Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ309005; CAC35209.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Eukaryota; Brachycera; Musc.

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc.

Ephydroidea; Drosophilidae; Drosophila.
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NON_TER 305 305

SEQUENCE 305 AA; 34028 MW; 572558C4B3634EE5 CRC64;
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SUP35.
                                                                                                                                                                  1029
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                      Local
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                      Q---GGYQQQFNPQGG-----
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                                                                   GYTPTYQNPFEGYHQPNQSSYQTNGGYQPPLPPHGGYQPPSQTYGGFQQPNRTYEDFHNP
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1149 SQTVGGFQPPYSVKGGYQPHNQLNGGYNQPNQSSSFQA-NGGYQPPSQ 1195

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RESULT 094079
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Best Local Similarity 38.1%;
Matches 51; Conservative
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MEDLIND=87286864; PubMed=3302672;

MEDLIND=87286864; PubMed=3302672;

Trueheart J., Boeke J.D., Fink G.R.;

Trueheart J., Boeke J.D., Fink G.R.;

True genes required for cell fusion during yeast conjugation: evidence for a pheromone-induced surface protein.";

MOI. Cell. Biol. 7:2316-2328(1987).

EMBL; M16717; AAA34615.1; -.

SEQUENCE 407 AA; 43262 MW; 6B26940F74A804C3 CRC64;
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O94079;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
YEAST (S.CEREVISIAE) FUS1 (FUSION GENE) AND BIK1 GENE REGION.
RNO1 AND YCLO28W.
Saccharomyces cerevisiae (Baker's yeast).
EUKBRYOLE; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
312 QOG-----QQQQQG 320
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Search completed: February Job time: 315 sec

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013354
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Q28009
P24639
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               bos taurus
bacillus th
caenorhabdi
drosophila
homo sapien
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bos taurus
dictyosteli
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triticum ae
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mus musculu
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schizosacch
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bacillus th
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caenorhabdi
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borrelia bu
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mus musculu	Q61545	EWS_MOUSE	Н	655	14.9	104.5	5
medicago fa	Q09134	GRPA_MEDFA	Н	159	14.9	104.5	44
triticum ae	P10387	GLTO_WHEAT	<u></u>	648	15.0	105.5	3
drosophila	Q08473	SQD_DROME	ب	345	15.0	105.5	42
triticum ae	P08488	GLT3_WHEAT		660	15.2	106.5	41
caenorhabdi	P34314	YKT3_CAEEL	ب	1231	15.3	107	0
caenorhabdi	P34291	YKO3_CAEEL	_	401	15.3	107	39
arabidopsis	004379	AGO1_ARATH	ب	1048	15.3	107.5	38
drosophila	P27781	CUP9_DROME	Ц	159	15.6	109.5	37
homo sapien	014497	SMF1_HUMAN	ب	1902	15.8	110.5	36
xenopus lae	P51989	RO21_XENLA	ب	346	15.8	110.5	ωs
caenorhabdi	010130	YSO5_CAEEL	Н	870	15.8	111	34

ALIGNMENTS

## RESPLYMARY REP2\_YEARY REP2\_YEARY REP2\_YEARY REP2\_YEARY REP2\_YEARY REP2\_YEARY REP2\_YEARY REP2\_REP2\_YEARY REP2\_REP2\_YE (OMNIPOTENT SUPPRESSOR of.

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F2_CANAL

DERF2_CANAL

C 01354;
C 013354;
C 013354;
T 15-JUL-1998 (Rel. 36, Created)
T 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR GTP-BINDING SUF
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Matches 123
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NP_BIND
NP_BIND
ACT_SITE
ACT_SITE
MOD_RES
CONFLICT
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The products of the SUP45 (eRF1) and SUP35 genes translation termination in Saccharomyces cerevisia EMBO J. 14:4365-4373(1995).
-1- FUNCTION: INVOLVED IN TRANSLATION TERMINATION.
           Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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The products of th
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BL; X07163; CAA30155.1; -.
BL; Y00829; CAA68760.1; -.
BL; Z46727; CAA86677.1; -.
R; S00733; EFBYS2.
SP; P02990; 1ETU.
SP; S0002579; SUP35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
SUBUNIT: HETERODIMER OF TWO SUBUNITS, ONE OF WHICH BINDS GTP.
SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                  MSDSNOGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                                                                                                                                              SQG
                                                                                                                                                                                                                                                                   QQYNDDAGYQQQYNDQGGYQQYNDQGGYQQQENDQGGRGNYKNFNYNNNLQGYQAGEQDQ
                                                                                                                                                                                                                                                                                                      MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                                                                                                                                                                       QQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00009; GTP_EFTU; 1.
TE; PS00301; EFACTOR_GTP;
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                135
249
685
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348
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76551
         Ascomycota; mitosporic
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EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      W.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEVERAL SORT OF REPEATS.

CHARGED.

TO ELONGATION FACTORS EF-1.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
INTERACT WITH GTP/GDP (BY SIMILARITY).
INTERACT WITH GTP/GDP (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
S -> C (IN REF. 4).

MW; 43912A6D77DFA153 CRC64;
                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                      Score 701; DB 1;
Pred. No. 1.5e-49;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation;
SEVERAL SORT OF R
          Saccharomycotina;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P35 genes interact to cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; GTP-binding.
REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
          Saccharomycetes;
; Candida.
                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 57
                                                                                                                                  RB56_HUMAN STANDARD; PKT; 332 km. 092804; 092751; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 7ATA-BINDING PROTEIN ASSOCIATED FACTOR 2N (RN. (TAFI168) (TAF(I1)68).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SIMILAR
NP_BIND
NP_BIND
NP_BIND
MOD_RES
SEQUENCE
SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
MEDLLINE-97124846; PubMed-8954779;
Morohoshi F., Arai K., Takahashi E.-I., Tanigami A.,
"Cloning and mapping of a human RBP56 gene encoding
binding protein similar to FUS/TLS and EWS proteins
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Resende C.G., Ferreira P.C., Tuite M.F., Duarte J.E.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ datal
1- FUNCTION: INVOLVED IN TRANSLATION TERMINATION.
ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                 TAF2N OR RBP56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-2005E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000795;
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                                                                                                                                                                                                                                                                                          GYQQYNSQPQQQ
                                                                                                                                                                                                                                                                                                                   GYQA-GFQPQSQ
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                                                                                                                                                                                                                                                                                                                                                                                             MANASLNGDQSKQQQQQQQQQQQQQQQV-----YYNPNAAQSFVPQGGYQQFQQFQPQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                     MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQ----PAGGY--YQNYQGYSG
                                                                                                                                                                                                                                                                                                                                           QQQYGGYNQYNQYQGGYQQNYNNRGGYQQGYNNRGGYQQNYN---NRGGYQGYNQNQQYG
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P02990; 1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00009; GTP_EFTU; 1.
TE; PS00301; EFACTOR_GTP;
in blosynthesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity
57; Conserv
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3 7 9 0 7 4 MW;
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                                                                                          Chordata;
Primates;
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8 SEVERAL SORT OF R
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
W; 740964B9561C49B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEVERAL SORT OF REPEATS CHARGED.
TO ELONGATION FACTORS I GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 228; DB 1;
Pred. No. 1.3e-11;
2; Mismatches 43
                                                                                          Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See
                                                                                           Hominidae;
                                                                                                                                                          (RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELONGATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 715;
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      = D
                                                                                                       Euteleostomi;
                            Ohki M.;
             putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY
                RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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Munakata M., Ohki M.;
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MEDLINE-97045110; E
                                                                       InterPro; IPR000504; InterPro; IPR001876;
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FUNCTION: RNA AND SSDNA-BINDING PROTEIN THAT MAY PLAY SPECIFIC ROLES DURING TRANSCRIPTION INTITATION AT DISTINCT PROMOTERS. CAN ENTER THE PREINITIATION COMPLEX TOGETHER WITH THE RNA POLYMERASE
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM AND A SHORT ISOFORM; ARE PRODUCED BY ALTERNATIVE
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AB010057; BAA33811.;
AB010058; BAA33811.;
AB010059; BAA33811.;
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                   PF00076; rrm; 1.
PF00641; zf-RanBP; 1.
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AB010061;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-91377317; PubMed-1897318;
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"The complete sequence of a 11,953 bp
"The complete sequence of a 11,953 bp
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Eukaryota; Fungi; Ascomycota; Saccharomyc
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[S,G](0,3)-G-G-Y+G-G.
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BIK1-FUS1 INTERGENIC
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01-NOV-1991 (Rel. 20
15-DEC-1998 (Rel. 37
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P23637;
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                                  Kushnirov V.V., Ter-Avanesyan M.D., D
Chernoff Y.O., Derkach I.L., Novikova
Neistat M.A., Tolstorukov I.I.;
"Divergence and conservation of SUP2
pinus and Saccharomyces cerevisiae.";
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"Two genes required for cell fusion during yeast conjugation:
evidence for a pheromone-induced surface protein.";
Mol. Cell. Biol. 7:2316-2328(1987).

-i- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION
                                                                                                                                                                                                                                                                               Eukaryota; Fung1; Ascomycota; Saccharomycetales; Saccharomycetales;
                                                                                                                                 MEDLINE=91181341; PubMed=2080663;
Kushnirov V.V., Ter-Avanesyan M.D.,
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Pichia pinus (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                PROTEIN
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                 Yeast
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                                                                                                                                                                                                                                                                                                                                                                                                         (TRANSLATION RELEASE
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[2]
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x59720; CAA42357.1; -.

C27061; C27061.

$19355; $19355.

$17471; $17471.
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                 6:461-472(1990).
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                                                                                                        Ter-Avanesyan M.D., Di
Derkach I.L., Novikova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=3302672; ke J.D., Fink G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                           20, Created)
20, Last sequence update)
37, Last annotation update)
E CHAIN RELEASE FACTOR GTP-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GRGNYKNFNYNNNLQGYQAGFQPQSQG
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181
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Pred. No. 7.4e-07;
7; Mismatches 44
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A -> T (IN REF. 2).
; 0629C40A7DE9C043 CRC64;
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                                                                                                        Didichenko
va O.N., Ing
                                                           (SUP35)
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                                                                                                           Inge-Vechtomov
                                                           gene
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(OMNIPOTENT SUPPRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                      Q28009;
01-NOV-1997
01-NOV-1997
20-AUG-2001
                                                                                 "A nuclear protein regulated during the transition quiescent phenotype in cultured endothelial cells." Dev. Biol. 174:288-297(1996).
regulatory protein, pigpen: new Exp. Cell Res. 255:270-277(2000)
          "A C-terminal carbohydrate-binding domain regulatory protein, pigpen: new function i
                                               MEDLINE-20160719;
                                                                                                                                                                                  Mammalia; Eutheri
Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed entities requires a license agreement (See
                                  Alliegro M.C.;
                                                             CARBOHYDRATE
                                                                                                                                                                                                                                                                                                                      FUS_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00009; GTP_EFTU; 1. PROSITE; PS00301; EFACTOR_GTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S12921; S12921.
HSSP; Q01698; 1TTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                   MEDLINE=96175600; PubMed=8631501;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                           RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                  TNSN-QGGYSNYN-----
                                                                                                                                                                                                                                                                                                                                                                                                         QQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNN---LQGYQAGF-----QPQSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQ 70
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45; Conserv
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                                                                                                                                                                                                          Eutheria;
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                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                   (Bovine).
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(Rel.
(Rel.
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312
325
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399
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                                                           BINDING
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                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                35, Created)
35, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                Bos.
                                               FubMed=10694442;
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311

741

332

406

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467

69

82373 MW;
                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                           FUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                           (PIGPEN
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CHARGED.
TO ELONGATION FACTORS
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
PHOSPHORVLATION (BY S.
PHOSPHORVLATION (BY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                           PROTEIN).
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           the an E
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           endothelial cell
EWS family member
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                                                                                                            active
                                                                                                                                                                                                           Bovoidea;
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Best Local Similarity
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InterPro; IPR001876; Znf-RanBP.
Pfam; PF00076; rrm; 1
Pfam; PF000641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
PROSITE; PS00030; RRM; 1.
PROSITE; PS00030; RRM, RNP_1; FALSE_NEG.
                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANNEXIN A7 (ANNEXIN VII) (SYNEXIN)
NXNA OR ANN7.
Dictyorphysical Control Cont
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ZN_FING
SEQUENCE
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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HSSP; P09651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                                                                                                                                                                                                            92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR, EXHI
SUBCELLULAR LOCATION: NUCLEOLI), TO
THROUGHOUT (EXCLUDING NUCLEOLI), TO
INTENSELY STAINED FOCAL POINTS, OR
ALONG THE NUCLEAR ENVELOPE.
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, OR GRANULES, AND PUNCTAT
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EMBL; X60270; CAA42815.1;
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EMBL; M69022; AAA33166.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Noegel A.A., Jacob U.;
"Crystel structure of the C-terminal tetrad repeat (annexin VII) of Dictyostellum discoideum.";
J. Mol. Biol. 270:79-88(1997).
I-FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS.
I-SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Identification
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Doring V., Schleicher M., Noegel A.A.;
"Dictyostelium annexin VII (synexin).
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InterPro; IPR001464; Annexin.
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OGYPPQQGYPPQQGYPPQQGYPPQQGYPPQQGYPPQQGYPPQ
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242 302 ANNEXIN 3.
324 384 ANNEXIN 3.
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STRAIN-ARCC 33530 / G-37;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270.397-403(1995).
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                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                  Score 143; DB
Pred. No. 4.8e
12; Mismatches
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                                                                                                                                                                                                                                                                        DB 1,
4.8e-05;
55;
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                                                                                                                                                                                                                                                                                                                               Length 372;
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20-AUG-2001
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between
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P56959;
                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND
-PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-
STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED
                                                                                                                                                                                                                                                Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
-!- SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUS.
                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000504; InterPro; IPR001876;
                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1353633;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF224264; AAF70602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alappat S.R.,
Burdsal C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                       RNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Regulation of pigpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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GGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                  GQQQSSYNPPQGYGQQNQYNSSSGGGGGGGGGGGNYGQDQSSMSGGGGGGGGGYGNQDQSGGGG
                                                         GYQQ - - YNPDAGY - - QQQYNPQ
                                                                                                      SDSNQGN--NQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQG-
                                                                                SQSSQSSYGQQSSYPGYGQQPAPSSTSGSYGGSSQSSSYGQPQSGGYGQQSGYGGQQQSY
                                                                                                                            l Similarity
46; Conserv
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278
364
421
518
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
PROTEIN FUS (PIGPEN PROTEIN).
                                                                                                                             Conservative
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29.1%;
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                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                     Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR RIBOPROTEIN COMPLEXES
                                                                                                                             12;
                                                                                                                                                                                   GLN/GLY/SER/TYR-RICH.
GLY-RICH.
RNA-BINDING (RRM).
ARG/GLY-RICH.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              is not removed.
                                                                                                                            Score 143; DB 1;
Pred. No. 6.5e-05;
2; Mismatches 60;
                                                                                                                                                                                                                                                                                FALSE_NEG
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in mouse embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alliegro M.A.,
                                                                                                                                                                                                                                                                     protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518
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            123
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                      CRC64;
                                                                                                                                                 Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alliegro
                                                                                                                             Indels
                                                                                                                                                                                                                                                                      Zinc-finger; Zinc;
                                                         -GGY----QQYNPQ 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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В

205

GGYGGGQQDRGGRGGGGGGYNRS----SGGYEPRGRG 238

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RESULT
SSXT_HUI
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Q15532; Q16404;
15-DEC-1998 (Re)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark J., Rocques P.J., Crew A.J., Gusterson B.A., Cooper C.S.; "Identification of novel genes, SYI t(X;18)(p11.2;q11.2) translocation Nat. Genet. 7:502-508(1994).
                                                  DOMAIN
SITE
DOMAIN
REPEAT
                         REPEAT
DOMAIN
                                                                                                          SITE
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                                                                                                                                                                                                              EMBL; X79201; CAA55792.1; ALT_INIT. EMBL; X79200; -; NOT_ANNOTATED_CDS. EMBL; S79894; AAB35674.1; ALT_TERM.
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
SEQUENCE
                                                                                                                                                                                                    MIM; 600192;
                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant SYT-SSX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 374-379 FROM N.A. (SS MEDLINE-96094743; Pubmed-7495284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSXT OR SYT.
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             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular diagnosis of synovial sarcoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95038836; PubMed=7951320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue=synovial sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SSXT-SSX2 FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    SYNOVIAL SARCOMAS AND IN OTHER HUMAN CELL LINES, THE FUSION GENE SSXT-SSX1 AND SSXT-SSX2 ARE EXPRESSED ONLY IN SYNOVIAL SARCOMAS. DISEASE: PARTICIPATES IN A T(x,18)(P11.2;011.2) CHROMOSOMAL TRANSLOCATION THAT IS SPECIFICALLY FOUND IN MORE THAN 80% OF SYNOVIAL SARCOMA AND PRODUCES THE SSXT-SSX1 OR SSXT-SSX2 FUSION PRODUCTS. THESE HYBRID PROTEINS ARE PROBABLY RESPONSIBLE FOR TRANSFORMING ACTIVITY. HETEROGENEITY IN THE POSITION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lant SYT-SSX2 fusion transcript.";
J. Pathol. 147:1592-1599(1995).
TISSUE SPECIFICITY: FAIRLY UBIQUITOUSLY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: STRONG, TO MOUSE SSXT.
                                                                                                                                                                                                                                                                                                                                                                                         BREAKPOINT CAN OCCUR
                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Lonardo F., Jhanwar S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
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343
361
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326
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                         (LOW FREQUENCY).
 ¥
                                                                                                                               Proto-oncogene; Repeat.
BREAKPOINT FOR TRANSLOCATION TO FORM THE
SSXT-SSX1 FUSION PROTEIN (RARE).
BREAKPOINT FOR TRANSLOCATION TO FORM THE
SSXT-SSX1 OR SSXT-SSX2 FUSION PROTEINS.
                                                                SH3-BINDING
SH2-BINDING
2 X 13 AA IM
                                                                                                     SH2-BINDING
SH2-BINDING
                          POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SSXT-SSX2 FUSION PROTEIN)
AlD64C2C588C532A CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tation update)
TRANSLOCATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gill S., Shipley J., Chan A.M.-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerald W.L., Woodruff
                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
                                                                                                     (POTENTIAL).
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                                                                              (POTENTIAL)
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SSXT_MOUSE
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Matches
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REPEAT
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SITE
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                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                  Oncogene 13:643-648(1996).

- I DEVELOPMENTAL STAGES: UBIQUITOUSLY EXPRESSED IN EARLY EMBRYOGENESIS
- I DAYS). IN LATER STAGES (14.5 DAYS), THE EXPRESSION IS
- I LATER STAGES (14.5 DAYS), THE EXPRESSION IS
- RESTRICTED TO CARTILAGE FORMING CELLS, TO SPECIFIC NEURONAL CELLS
- RESTRICTED TO CARTILAGE FORMING CELLS, TO SPECIFIC NEURONAL CELLS
- AND SOME EPITHELIAL DERIVED TISSUES. IN ADULTS, SSTX IS EXPRESSED
- IN HEART, KIDNEY, TESTIS AND ALSO IN MUSCLE, BRAIN AND LIVER. IN
- MATURE TESTIS, EXPRESSION IS SPECIFICALLY OBSERVED IN PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                Olde Weghuis D., Hirning-Folz U., Geurts van Kessel A.G., "Isolation and characterization of the mouse homolog of S implicated in the development of human synovial sarcomas.
                           REPEAT
DOMAIN
                                                                                                                                        MGD;
                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Bruijn D.R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129; TISSUE-Fetal brain; MEDLINE-96330344; PubMed-8760306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSXT OR SYT
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15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSXT_MOUSE
                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998
20-AUG-2001
SEQUENCE
              DOMAIN
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(Rel.
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37, Last sequence update)
40, Last annotation update
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35.7%;
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MW;
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Pred. No. 7
              POLY-GLN
                           POLY-PRO
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D32BE6AD97396CA2 CRC64;
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(PERFECT TANDEM REPEATS.
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homolog of SYT,
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Query Match Best Local Similarity

19.8%;

Score Pred.

139; DB 1; No. 0.00011;

Length 418;

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   Ichikawa H., Shimlzu K., Hayashi Y., Ohki M.;
"An RNA-binding protein gene, TLS/FUS, is fused to ERG in human myeloid leukemia with t(16;21) chromosomal translocation.";
Cancer Res. 54:2865-2868(1994).
"In FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994
20-AUG-2001
RNA-BINDING
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novel gene
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                                                                                                                                                        "Human P., Akhmedov A.T., Delacote F., Durrbach A., Lo
"Human POMp75 is identified as the pro-oncogene TLF/FUS:
POMp75 and POMp100 DNA homologous pairing activities are
to cell prolifieration.";
Oncogene 18:4515-4521(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Morohoshi F., Ootsuka Y., Arai K., Ichikawa H., Munakata N., Ohki M.; "Genomic structure of the human RBP56/hTAFII68 Gene 221:191-198(1998).
                                                                                                                                                                                                                                                                                                                Baechtold H., Kuroda M., Sok J., Ron D., Lopez B.S., / "Human 75-kba DNA-pairing protein is identical to the "LS.FUS and is able to promote D-loop formation."; J. Biol. Chem. 274:34337-34342(1999).
                                                                                                     MEDLINE=94243799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG AND SHORT MEDLINE=99013873; PubMed=9795213;
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MEDLINE=93288139; Pubmed=8510758;
Crozat A., Aman P., Mandahl N., Ron D.;
"Fusion of CHOP to a novel RNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crozat A., Aman
"Fusion of CHOP
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                           MEDLINE=99369251;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 235-244; 307-312;
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(Rel. 40, Last annotation update)
PROTEIN FUS (ONCOGENE FUS) (ONCOGENE TLS) (TRANSLOCATED
PROTEIN) (POMP75) (75 KDA DNA-PAIRING PROTEIN)
                                                                                                                        TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H., Forster A., Larson R., Nathan P.;
the dominant negative transcription regulator CHOP with a
FUS by translocation t(12;16) in malignant liposarcoma.";
4:175-180(1993).
                                                                                                                                                                                                                                                                             265-276; 317-331
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PubMed=10442642;
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Catarrhini;
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                                                                                                                                                                                                                                                                           IDENTIFICATION
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InterPro; IPR001876; Znf-RanE
Pfam; PF00076; rrm; 1.
Pfam; PF000641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
PROSITE; PS50102; RRM; 1.
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EMBL; AF071213; AAC35;
PIR; S33799; S33799.
HSSP; P09651; 1HA1.
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CONFLICT
SEQUENCE
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ZN_FING
SITE
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STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED
DNA, MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY.

-!- SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- ALTERNATIVE PRODUCCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)
AND A SHORT ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: UBLQUITOUS.

-!- TISSUE SPECIFICITY: UBLQUITOUS.

-!- DISEASE: A FORM OF MALIGNANT MYXOID LIPOSARCOMA IS CHARACTERIZED
BY A CHROMOSOMAL TRANSLOCATION T(12;16)(Q13;P11) THAT INVOLVES FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proto-oncogene;
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SIMILARITY:
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DISEASE: A FORM OF ACUTE
BY A CHROMOSOMAL TRANSLOC
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S62138; AAB27103.1;
X71427; CAA50558.1;
X71428; CAA50559.1;
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YQQYNPQGGY--QQQENPQ---
                                                                                                                                                                     SNQGNNQQNYQQYSQNGNQQ-QGNNRYQGY-----QAYNAQAQP-----AGGY-----
                                                      SSYGQQSSYPGYGQQPAPSSTSGSYGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQ--
                                                                                                                                SSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSTGGYGSSQSSQ
                                                                                                                                                                                                                            Similarity
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338
526
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285
371
422
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                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC35285.1;
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267
371
526
453
267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Znf-RanBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _RNP_1; FALSE_NEG.
inding; DNA-binding; Nuclear protein; Rei
Chromosomal translocation; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1; ALT_SEQ.
8.1; ALT_SEQ.
9.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                      MW.
                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                    TG -> S (IN SHORT ISON T -> N (IN REF. 4).
                                                                                                                                                                                                                            Score 136;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                  GLN/GLY/SER/TYR-RICH.
GLY-RICH.
RNA-BINDING (RRM).
ARG/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                             RANBP-TYPE.
BREAKPOINT FOR TRANSLOCATION
-GGRGNY---
                                                                                                                                                                                                                                                                                                      -> N (IN REF. 4).
88C8E263B7905549
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                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                            00024;
                                                                                                                                                                                                                                                DB
                                                                                           QQGGYQQYNPDAGYQQQYNPQGG
                                                                                                                                                                                                           57;
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                 ----KNFNYNNNLQ----GYQ
                                                                                                                                                                                                                                                                                                                                           ISOFORM).
                                                                                                                                                                                                                                          Length 526
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Best Local S
Matches 44
                                                                                  IF2_BORBU STANDARD; PRT; 882 AA 051741; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TRANSLATION INITIATION FACTOR IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
YEM6_YEAST
                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 14.6 KDA PROTEIN IN TTP1-KAP104
MEDLINE-98065943; PubMed-9403685; Mention M. Castens S., Huang W.M.,
                   SEQUENCE FROM N.A. STRAIN-ATCC 35210
                                                         Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                              EMBL; Z35885; CAA84958.1;
PIR; S45871; S45871.
SGD; S0000220; YBR016W.
                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YBR016W OR YBR0222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994
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                                                                             INFB OR BB0801.
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                                               NCBI_TaxID-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                               128 AA; 1
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s E., Miosga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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. 30, Last sequence 35, Last annotation
                                                                                                                                                                                   - QGY NQQGY NQQGHQQPVY VQQQPPQ - - RGN
                     / B31;
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40.7%;
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                                                        Spirochaetaceae;
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                                                                                                                                                                                                                                                              Score 135; DB 1;
Pred. No. 7.6e-05;
4; Mismatches 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                  spirochete)
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  Sutton
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G.G.,
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                                                                                                                                                                                                                                                                                 Length 128;
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  Clayton R.A.,
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DOMAIN
                            HNRPD OR AUF1
                                      RNA-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR;
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389
435
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Query Match
Best Local Similarity
                                                                                                                                                                                                        ROD_RAT STANDARD; PRT; 353 AA. | 09JJ54; Q9JJ552; Q9JJ551; Q9JJ552; Q9JJ52; Q9J
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam; PF02131; IF2; 1.
ProDom; PD186100; IF2; 1.
PROSITE; PS01176; IF2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORMYLMETHIONYL-TRNA FROM SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BUNDING TO THE 30S RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY)
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Utterback T., Watthey L., McDonald L., Artiac Garland S., Fujii C., Cotton M.D., Horst K., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lathigra R., White O., Ket Dougherty B., Tomb J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001179; AAC67153.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, SDSNQG---NNQQNYQQYSQN-----GNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRDNRTGGYSQ-NRDNRTGGY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-GYQQ-----GGYQQY--NPDAGYQQQYNPQGGYQQ--YNPQGGY-QQQFNPQGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGYSQNRDNRTGGYSQNRDNRTGGYSQNRDNRGGYSQGRDNRTGGYSQ
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                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 132; DB 1;
Pred. No. 0.00082
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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    Craniata; Ver
Sciurognathi;
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                                           Vertebrata;
                                                                                                                                                                                                                 (HNRNP
        Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts K., Hatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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    Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                 (AU-RICH
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D.,
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Best Local Similarity 38.3
Matches 30; Conservative
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VARSPLIC
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 2
Nuclear protein; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB046615; BAB03465.1; -. EMBL; AB046616; BAB03467.1; -. EMBL; AB046617; BAB03467.1; -. EMBL; AB046618; BAB03468.1; -. InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-Kidney; Arao Y., Kikuchi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116; [1]
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                                                                                                                                 335 SGYGKVSRRGGHQNSYKP 352
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345
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                                                                                                                                                                                                                                                                                                                                                                   18.3%;
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; 6190EE1006F07DCB CRC64;
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RNA-BINDING (RRM) 2.

GLY-RICH.

TYR-RICH.

MISSING (IN ISOFORM 2 AND ISOFORM 4).

GPSQNWNQGYSNYWNQGYGSYGYNSQGYGGYDYTGYNS

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                                                                                                                                                                                                                                          GSYGYNSQGYGGYGYDYTGYNSYYGYGDYSNQQ 334
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